

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:41:05 ; Search time 18 seconds  
(without alignments)  
1310.432 Million cell updates/sec

Title: US-09-846-512-2  
Perfect score: 2443  
Sequence: 1 MGNDPFAVAPFSLFG.....TRVTSFLDWHQMERDLKT 453

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score  | Query Match | Length | DB ID        | Description         |
|------------|--------|-------------|--------|--------------|---------------------|
| 1          | 2432.5 | 99.6        | 454    | 1 TMS3_HUMAN | P57727 homo sapien  |
| 2          | 2226   | 91.1        | 453    | 1 TMS3_MOUSE | O8k1c0 mus musculus |
| 3          | 982    | 36.1        | 492    | 1 TMS2_HUMAN | O15393 homo sapien  |
| 4          | 875    | 35.8        | 490    | 1 TMS2_MOUSE | Q9j1q8 mus musculus |
| 5          | 695.5  | 28.5        | 455    | 1 TMS5_MOUSE | Q9h044 mus musculus |
| 6          | 689.5  | 28.2        | 457    | 1 TMS5_HUMAN | Q9h363 homo sapien  |
| 7          | 677    | 27.7        | 435    | 1 TMS4_MOUSE | O8vca5 mus musculus |
| 8          | 674    | 27.6        | 417    | 1 HEP5_HUMAN | P05381 homo sapien  |
| 9          | 669.5  | 27.4        | 1035   | 1 ENTK_BOVIN | P98072 bos taurus   |
| 10         | 664.5  | 27.2        | 1019   | 1 ENTK_HUMAN | P98073 homo sapien  |
| 11         | 663.5  | 27.2        | 1034   | 1 ENTK_PIG   | P98074 sus scrofa   |
| 12         | 659.5  | 27.0        | 436    | 1 HEP5_MOUSE | O35453 mus musculus |
| 13         | 658    | 26.9        | 437    | 1 TMS4_HUMAN | Q9nrs4 homo sapien  |
| 14         | 654.5  | 26.8        | 416    | 1 HEP5_RAT   | Q05511 rattus norv  |
| 15         | 651    | 26.6        | 1069   | 1 ENTK_MOUSE | P97435 mus musculus |
| 16         | 579.5  | 23.7        | 638    | 1 KAL_RAT    | P14272 rattus norv  |
| 17         | 578.5  | 23.7        | 811    | 1 TMS6_MOUSE | Q9db10 mus musculus |
| 18         | 571    | 23.4        | 418    | 1 HATT_HUMAN | P26262 homo sapien  |
| 19         | 570.5  | 23.4        | 638    | 1 KAL_MOUSE  | O60335 mus musculus |
| 20         | 560    | 22.9        | 811    | 1 TMS6_HUMAN | Q81u80 homo sapien  |
| 21         | 549.5  | 22.5        | 638    | 1 KAL_HUMAN  | P03952 homo sapien  |
| 22         | 543.5  | 22.2        | 855    | 1 ST14_HUMAN | Q9y3y6 homo sapien  |
| 23         | 532.5  | 21.8        | 324    | 1 TEST_MOUSE | Q9j1j7 mus musculus |
| 24         | 527    | 21.6        | 761    | 1 NETR_MOUSE | O08762 mus musculus |
| 25         | 526    | 21.5        | 330    | 1 PLMN_HORSE | P80010 equus caball |
| 26         | 523.5  | 21.4        | 798    | 1 PLMN_PIG   | P06867 sus scrofa   |
| 27         | 523    | 21.4        | 855    | 1 ST14_MOUSE | P56677 mus musculus |
| 28         | 522.5  | 21.4        | 422    | 1 DES1_HUMAN | Q9u152 homo sapien  |
| 29         | 520.5  | 21.3        | 1042   | 1 COR1_HUMAN | Q9y5g5 homo sapien  |
| 30         | 511.5  | 20.9        | 311    | 1 TRY3_MOUSE | Q9q1l7 mus musculus |
| 31         | 507    | 20.8        | 314    | 1 TEST_HUMAN | Q9y6m0 homo sapien  |
| 32         | 506.5  | 20.7        | 1113   | 1 COR1_MOUSE | Q9z319 mus musculus |
| 33         | 505    | 20.7        | 875    | 1 NETR_HUMAN | P56730 homo sapien  |

|    |       |      |     |              |                     |
|----|-------|------|-----|--------------|---------------------|
| 34 | 504   | 20.6 | 273 | 1 MCT7_MOUSE | Q02844 mus musculus |
| 35 | 504   | 20.6 | 625 | 1 FAL1_HUMAN | P03951 homo sapien  |
| 36 | 502   | 20.5 | 275 | 1 TRY1_CANFA | P15944 canis faml   |
| 37 | 502   | 20.5 | 810 | 1 PLMN_HUMAN | P00747 homo sapien  |
| 38 | 502   | 20.5 | 812 | 1 PLMN_MOUSE | P20918 mus musculus |
| 39 | 500.5 | 20.5 | 343 | 1 PLMN_SHEEP | P81286 ovis aries   |
| 40 | 499   | 20.4 | 273 | 1 TRY1_SHEEP | Q9xsm2 ovis aries   |
| 41 | 499   | 20.4 | 810 | 1 PLMN_ERIEU | Q29485 erinaceus e  |
| 42 | 495.5 | 20.3 | 437 | 1 ACRO_RAT   | P29293 rattus norv  |
| 43 | 495   | 20.3 | 270 | 1 TRY1_MERUN | P50342 meriones un  |
| 44 | 495   | 20.3 | 810 | 1 PLMN_MACMU | P12345 macaca mula  |
| 45 | 495   | 20.3 | 812 | 1 PLMN_BOVIN | P06868 bos taurus   |

ALIGNMENTS

RESULT 1  
TMS3\_HUMAN  
ID TMS3\_HUMAN STANDARD; PRT; 454 AA.  
AC P57727;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Transmembrane protease, serine 3 (PC 3.4.21.-) (Serine protease  
TAG-12) (Tumor associated differentially-expressed gene-12 protein).  
GN TMS3 OR TAG12 OR ECHS1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A. (ISOFORMS A AND T).  
RC TISSUE=Ovarian carcinoma;  
RX MEDLINE=20521358; PubMed=11068177;  
RA Underwood L.J., Shigenaga K., Imanoto H., Beard J.B., Schneider E.N.,  
Wang Y., Parmley T.H., O'Brien T.J.;  
RT "Ovarian tumor cells express a novel multi-domain cell surface serine  
protease";  
RL Biochim. Biophys. Acta 1502:337-350(2000).  
[2]  
RN SEQUENCE FROM N.A. (ISOFORMS A; B AND D), AND VARIANT ILE-53.  
RX MEDLINE=20578749; PubMed=11137999;  
RA Scott H.S., Kidoh J., Wattenhofer M., Shibuya K., Berry A., Chrast R.,  
Guipponi M., Wang J., Kawasaki K., Asakawa S., Minoshima S.,  
Younis F., Mehdi S.O., Radhakrishna U., Papasavvas M.P., Gehrig C.,  
Rossier C., Korostishevsky M., Gal A., Shimizu N., Bonne-Tamir B.,  
Antonarakis S.E.;  
RT "Insertion of beta-satellite repeats identifies a transmembrane  
protease causing both congenital and childhood onset autosomal  
recessive deafness";  
RL Nat. Genet. 27:59-63(2001).  
[3]  
RN SUBCELLULAR LOCATION, AND FUNCTION IN ENAC CLEAVAGE.  
RX MEDLINE=2281255; PubMed=12393794;  
RA Guipponi M., Vuagniaux G., Wattenhofer M., Shibuya K., Vazquez M.,  
Dougherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M.,  
Bucht K., Raymond A., Hummler B., Marzella P.L., Kidoh J.,  
Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.;  
RT "The transmembrane serine protease (TMS3) mutated in deafness  
DNBS10 activates the epithelial sodium channel (ENAC) in vitro.";  
RL Hum. Mol. Genet. 11:2829-2836(2002).  
[4]  
RN VARIANTS DNBS10 CYS-251 AND LEU-404.  
RX MEDLINE=21354482; PubMed=11462234;  
RA Masoudi S., Antonarakis S.E., Schwede T., Ghorbel A.M., Gratri M.,  
Papavasavas M.P., Drira M., Elgaied-Boullila A., Wattenhofer M.,  
Rossier C., Scott H.S., Ayadi H., Guipponi M.;  
RT "Novel massive mutations of TMS3 in two consanguineous Tunisian  
families with non-syndromic autosomal recessive deafness";  
RL Hum. Mutat. 18:101-108(2001).  
[5]  
RN VARIANTS DNBS10 TRP-109; PHE-194 AND ARG-407, AND VARIANTS

RP ILE-53; SER-111 AND VAL-253.  
RX MEDLINE-21317610; PubMed-11424922;  
RA Ben-Yosef T., Wattenhofer M., Riazuddin S., Ahmed Z.M., Scott H.S.,  
RA Kudoh J., Shibuya K., Antonarakis S.E., Bonne-Tamir B.,  
RA Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A.,  
RA Nance W.B., Wilcox E.R., Friedman T.B., Morell R.J.;  
RT "Novel mutations of TMPSR3 in four DFNB8/B10 families segregating  
RT congenital autosomal recessive deafness.";  
RL J. Med. Genet. 38:396-400(2001).  
RN [6]  
RP VARIANT DFNB8/DFNB10 GLY-103, AND VARIANTS ASN-173 AND THR-426.  
RX MEDLINE-21904597; PubMed-11907649;  
RA Wattenhofer M., Di Iorio V., Radonnet R., Dougherty L., Pampalos A.,  
RA Schwede T., Montserrat-Sentis B., Arbones L., Illades T.,  
RA Pasquadi Bisceglie A., D'Amelio M., Alwan S., Rossier C., Dahl H.-H.M.,  
RA Petersen M.B., Estivill X., Gasparini P., Scott H.S.,  
RA Antonarakis S.E.;  
RT "Mutations in the TMPSR3 gene are a rare cause of childhood  
RT nonsyndromic deafness in Caucasian patients.";  
RL J. Mol. Med. 80:124-131(2002).  
CC -1- FUNCTION: Probable protease. Seems to be capable of activating  
CC ENAC.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic  
CC reticulum.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=4;  
CC Name=A;  
CC IsoId=P57727-1; Sequence=VSP\_005391;  
CC Name=B; Synonyms=C;  
CC IsoId=P57727-2; Sequence=VSP\_005391;  
CC Name=D;  
CC IsoId=P57727-3; Sequence=VSP\_005392;  
CC Name=T; Synonyms=Truncated, TAG-12V;  
CC IsoId=P57727-4; Sequence=VSP\_005393, VSP\_005394;  
CC -1- TISSUE SPECIFICITY: Expressed in many tissues including fetal  
CC cochlea. Isoform T is found at increased levels in some  
CC carcinomas.  
CC -1- PTM: Undergoes autophosphorylation.  
CC -1- DISEASE: Defects in TMPSR3 are a cause of childhood-onset  
CC autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072].  
CC -1- DISEASE: Defects in TMPSR3 are a cause of congenital autosomal  
CC recessive neurosensory deafness 10 (DFNB10) [MIM:605316].  
CC -1- SIMILARITY: Belongs to peptidase family 11.  
CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.  
CC -1- SIMILARITY: Contains 1 SRCR domain.  
CC -----  
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CC -----  
DR EMBL; AF201380; AAC37012.1; -  
DR EMBL; AB038157; BAB20077.1; -  
DR EMBL; AB038158; BAB20078.1; -  
DR EMBL; AB038159; BAB20079.1; -  
DR EMBL; AB038160; BAB20080.1; -  
DR HSSP; P00763; 1DPO.  
DR MEROPS; S01.079; -  
DR Genbank; HGNC:11677; TMPSR3.  
DR MIM; 605511; -  
DR MIM; 601072; -  
DR MIM; 605316; -  
DR MIM; 605316; -  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; Cys Ser trypsin.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR001190; Srcr\_receptor.

DR Pfam; PF00057; ldl\_recept\_a; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SMC0192; LDLa; 1.  
DR SMART; SMC0202; SR; 1.  
DR SMART; SMC0202; TRY\_SPC; 1.  
DR PROSITE; PS01209; LDLRA\_1; 1.  
DR PROSITE; PS00668; LDLRA\_2; 1.  
DR PROSITE; PS00420; SRCR\_1; FALSE\_NEG.  
DR PROSITE; PS0287; SRCR\_2; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS0134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00138; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen;  
KW Endoplasmic reticulum; Deafness; Alternative splicing;  
KW Disease mutation; Polymorphism.  
FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT FT (POTENTIAL).  
FT FT EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 70 454 LDL-RECEPTOR CLASS A.  
FT DOMAIN 72 108 SRCR.  
FT DOMAIN 109 205 SERINE PROTEASE.  
FT ACT\_SITE 217 454 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 257 257 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 304 304 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 401 401 CLEAVAGE (POTENTIAL).  
FT SITE 216 217 BY SIMILARITY.  
FT DISULFID 73 85 BY SIMILARITY.  
FT DISULFID 79 98 BY SIMILARITY.  
FT DISULFID 92 107 BY SIMILARITY.  
FT DISULFID 129 194 BY SIMILARITY.  
FT DISULFID 142 204 BY SIMILARITY.  
FT DISULFID 207 324 BY SIMILARITY.  
FT DISULFID 242 258 BY SIMILARITY.  
FT DISULFID 338 407 BY SIMILARITY.  
FT DISULFID 370 386 BY SIMILARITY.  
FT DISULFID 397 425 BY SIMILARITY.  
FT CARBOHYD 221 127 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 1 127 Missing (in isoform B).  
FT FT (FTID=VSP\_005391).  
FT EMIQVCLPNSSENFDPGKVCWTSGWATGAGDAGSPVLN  
FT HAAVPLNCKHNRDVGIIISPMICAGVLTGGVSCQG  
FT DSGGLVCOERLKLKVGATSGFGCAEVNKPVTYRTVSF  
FT LDMTHQWERDLKT -> GTSGSLCGSAALPLFQEDLQLLI  
FT EAPL (in isoform D).  
FT FTID=VSP\_005392.  
FT FT (FTID=VSP\_005393).  
FT PRERADRRGRKLLCWKPKTKMKGRPSHS (in isoform  
FT T).  
FT FTID=VSP\_005393.  
FT Missing (in isoform T).  
FT FTID=VSP\_005394.  
FT V -> I.  
FT FTID=VAR\_010781.  
FT D -> G (in DFNB8/DFNB10).  
FT FTID=VAR\_013490.  
FT R -> W (in DFNB8/DFNB10).  
FT FTID=VAR\_013491.  
FT G -> S.  
FT FTID=VAR\_013492.  
FT D -> N.  
FT FTID=VAR\_013493.  
FT C -> F (in DFNB8/DFNB10).  
FT FTID=VAR\_013494.  
FT W -> C (in DFNB8/DFNB10).  
FT FTID=VAR\_011678.  
FT I -> V (in dbSNP:2839500).  
FT FTID=VAR\_013101.  
FT P -> L (in DFNB8/DFNB10).  
FT FTID=VAR\_011679.  
FT C -> R (in DFNB8/DFNB10).  
FT FTID=VAR\_013495.  
FT A -> T.

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|  |
|--|
| EMBL; AJ49216; CAD22137.1; -;                      |
| EMBL; AJ300738; CAC83350.1; -;                     |
| HSSP; P00761; IAN1.                                |
| MGD; MGI:2155445; Tmprs3.                          |
| InterPro; IPRO09003; Cys_Ser_trypsin.              |
| InterPro; IPRO02172; LDL_receptor_A.               |
| InterPro; IPRO01254; Peptidase_S1                  |
| InterPro; IPRO01114; Peptidase_SIA.                |
| InterPro; IPRO01190; Sctr_receptor.                |
| Pfam; PF00057; ldl_recept_2; 1.                    |
| Pfam; PF00089; trypsin; 1.                         |
| PRINTS; PR00722; CHYMOTRYPSIN.                     |
| SMART; SM00193; LDLa; 1.                           |
| SMART; SM00203; SR; 1.                             |
| SMART; SM00020; TRYP_SPC; 1.                       |
| PROSITE; PS01209; LIDRA_1; 1.                      |
| PROSITE; PS00688; LDLRA_2; 1.                      |
| PROSITE; PS03887; SRCR_2; 1.                       |
| PROSITE; PS00440; TRYPSIN_DOM; 1.                  |
| PROSITE; PS00134; TRYPSIN_HIS; 1.                  |
| PROSITE; PS00135; TRYPSIN_SER; 1.                  |
| Hydrolase; Serine protease; Zymogen;               |
| Endoplasmic reticulum.                             |
| DOMAIN 1 48  |
| TRANSMEM 49 69                                     |
| DOMAIN 70 453                                      |
| DOMAIN 72 108                                      |
| DOMAIN 104 205                                     |
| DOMAIN 217 448                                     |
| ACT_SITE 257 257                                   |
| ACT_SITE 304 304                                   |
| ACT_SITE 400 400                                   |
| SITE 215 217                                       |
| DISULFID 73 85                                     |
| DISULFID 79 98                                     |
| DISULFID 92 107                                    |
| DISULFID 129 194                                   |
| DISULFID 142 204                                   |
| DISULFID 207 324                                   |
| DISULFID 242 258                                   |
| DISULFID 338 406                                   |
| DISULFID 369 385                                   |
| DISULFID 396 424                                   |
| CARBOHYD 121 221                                   |
| CONFLICT 117 117                                   |
| CONFLICT 246 246                                   |
| SEQUENCE 453 AA; 49491 MW; 1ABCBF10A76E1EF6 CRC64; |

|     | Query Match  | 91.1%            | Score 2226;         | DB 1;     | Length 453; |
|-----|--|------------------|---------------------|-----------|-------------|
|     | Best Local Similarity  | 89.2%;           | Pred. No. 8.1e-181; |           |             |
|     | Matches 404;   | Conservative 24; | Mismatches 25;      | Indels 0; | Gaps 0      |
| 1   | MGENDPAAVEAPPSFSLFGLDDLKISVPAPADAAVAAQILSLLPLKFPPIIVIGIIALI  | 60               |                     |           |             |
| 1   | MGENDPPAAEAPPSFSLFGLDDLKISVPAPQGDAAVAAQILSLLPLKFPPIIVIGIIALI | 60               |                     |           |             |
| 61  | LALAIGLGIHFDCSGKYRCSSFKELIARCDGVSDCKGDEYRCVVGQNAVLQVF        | 120              |                     |           |             |
| 61  | LALAIGLGIHFDCSGKYRCHRSFKELIARCDGVSDCKNADEYRCVMSGRAALQVF      | 120              |                     |           |             |
| 121 | TAAASWTCMSDDWKGHYANVACAAQLGFPSPVSSDNLRVSLGQFEEFVSDIHLPLDDK   | 180              |                     |           |             |
| 121 | TAAAWRTCMSDDWKSHYAKIACAAQLGFPSPVSSDHLRVDALEEQFGDFVSNHLLSDK   | 180              |                     |           |             |

| Query Match           | 99.68; | Score           | 2432.5;              | DB 1;                               | Length    | 454; |    |
|-----------------------|--------|-----------------|----------------------|-------------------------------------|-----------|------|----|
| Best Local Similarity | 99.8;  | Prod.           | No. 2.7e-198;        |                                     |           |      |    |
| Matches               | 453;   | Conservative    | 0;                   | Mismatches                          | 1;        | Gaps | 1; |
| QY                    | 1      | MGNDPPAVEAPF    | FRSLGLGLDDIKTS       | PVAPFDADAVAAQILSLPLKFPFI            | IVIGIIALI | 60   |    |
| DB                    | 1      | MGNDPPAVEAPF    | FRSLGLGLDDIKTS       | PVAPFDADAVAAQILSLPLKFPFI            | IVIGIIALI | 60   |    |
| QY                    | 61     | LALAILGLGIH     | FDGSKYKRCSSFKCIELI   | ARCQGVSDCKDGDGEYRCVRVGQONAVLQVF     | 120       |      |    |
| DB                    | 61     | LALAILGLGIH     | FDGSKYKRCSSFKCIELI   | ARCQGVSDCKDGDGEYRCVRVGQONAVLQVF     | 120       |      |    |
| QY                    | 121    | TAAASWKTWCS     | DDWKXGHYANVACA       | GLGFPFVSVDNLRVSLSEQCFREEFVSDIHLPLDK | 180       |      |    |
| DB                    | 121    | TAAASWKTWCS     | DDWKXGHYANVACA       | GLGFPFVSVDNLRVSLSEQCFREEFVSDIHLPLDK | 180       |      |    |
| QY                    | 181    | VTALHSYVY       | REGCASHVVTLOCTA      | CHGRGVSSRIVGNNWLLSOWPQASLQFGVH      | 240       |      |    |
| DB                    | 181    | VTALHSYVY       | REGCASHVVTLOCTA      | CHGRGVSSRIVGNNWLLSOWPQASLQFGVH      | 240       |      |    |
| QY                    | 241    | LCGGSVITPLMTII  | TAACHCVYDYLXPKS      | WTIQVGLVSLDDNPNAPSHLVEKIVYHSKYKPKR  | 300       |      |    |
| DB                    | 241    | LCGGSVITPLMTII  | TAACHCVYDYLXPKS      | WTIQVGLVSLDDNPNAPSHLVEKIVYHSKYKPKR  | 300       |      |    |
| QY                    | 301    | LGNDIALMKLAGPLT | FNEMIOVCLPNSEENFP    | DGKVCWTSGHGATEDG- GDASPVINHA        | 359       |      |    |
| DB                    | 301    | LGNDIALMKLAGPLT | FNEMIOVCLPNSEENFP    | DGKVCWTSGHGATEDG- GDASPVINHA        | 360       |      |    |
| QY                    | 360    | AVPLISNKNICNHRD | YVYGIISPSMLCAGYLT    | GGVDSQQGDSGGPLVCQFRRRLWKLVGATS      | 419       |      |    |
| DB                    | 361    | AVPLISNKNICNHRD | YVYGIISPSMLCAGYLT    | GGVDSQQGDSGGPLVCQFRRRLWKLVGATS      | 420       |      |    |
| QY                    | 420    | FIGICAEVNVKPGVY | TRVTSFLDWTHEQMERDLKT | 453                                 |           |      |    |
| DB                    | 421    | FIGICAEVNVKPGVY | TRVTSFLDWTHEQMERDLKT | 454                                 |           |      |    |

RESULT 2

|                   |   |      |         |
|-------------------|---|------|---------|
| TM3S_MOUSE        | STANDARD;   | PRT; | 453 AA. |
| ID                | TM3S_MOUSE  |      |         |
| AC                | Q8K1T0; Q8VDE0;   |      |         |
| DT                | 10-OCT-2003 (Rel. 42, C-created)                                      |      |         |
| DT                | 10-OCT-2003 (Rel. 42, Last sequence update)                           |      |         |
| DT                | 13-MAR-2004 (Rel. 43, Last annotation update)                         |      |         |
| DE                | Transmembrane protease, serine 3 (EC 3.4.21.-).                       |      |         |
| GN                | TMPRSS3.  |      |         |
| OS                | Mus musculus (Mouse).   |      |         |
| OC                | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;               |      |         |
| OC                | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.    |      |         |
| NCBI_TaxID=10090; |   |      |         |
| EN                | [1]   |      |         |
| RP                | SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND FUNCTION IN ENAC        |      |         |
| RP                | CLEAVAGE.   |      |         |
| RX                | MEDLINE=22281255; PubMed=12393794;                                    |      |         |
| RA                | Guipponi M., Vuagniaux G., Wattenhofer M., Shibuya K., Vazquez M.,    |      |         |
| RA                | Dougherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M., |      |         |
| RA                | Buchet K., Raymond A., Hummler E., Marzella P.L., Kudoh J.,           |      |         |
| RA                | Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.;               |      |         |
| RT                | "The transmembrane serine protease (TMPRSS3) mutated in deafness      |      |         |
| RT                | DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro.";   |      |         |
| RL                | Hum. Mol. Genet. 11:2829-2836(2002).                                  |      |         |
| CC                | -!- FUNCTION: Probable protease. Seems to be capable of activating    |      |         |
| CC                | ENaC.   |      |         |
| CC                | -!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic       |      |         |
| CC                | reticulum.  |      |         |
| CC                | -!- TISSUE SPECIFICITY: Expressed in the spiral ganglion, the cells   |      |         |
| CC                | supporting the organ of Corti and the stria vascularis.               |      |         |
| CC                | -!- PTM: Undergoes autophoretic activation.                           |      |         |
| CC                | -!- SIMILARITY: Belongs to peptidase family S1.                       |      |         |
| CC                | -!- SIMILARITY: Contains 1 LDL-receptor class A domain.               |      |         |
| CC                | -!- SIMILARITY: Contains 1 SRCR domain.                               |      |         |

QY 181 VTALHSHVYVREGGASGHVTVLQCTACHRRGYSRIVGNGMSSLQWQASLQFGQYH 240  
DQ 181 VTALHSHVYVREGGASGHVTVLQCTACHRRGYSRIVGNGMSSLQWQASLQFGQYH 240  
QY 241 LCGGSVITPLMIITAAHCVYDYLKPKSWTIOGLVSLIDNPAPSHLVEKIVHSHKYPKR 300  
DQ 241 LCGGSVITPLMIITAAHCVYDYLKPKSWTIOGLVSLIDNPAPSHLVEKIVHSHKYPKR 300  
QY 301 LGNIALMKLAGPTFTNEMIPVCLPNSSENFPGKVCWTSGWGTGDDGASPVLNAA 360  
DQ 301 LGNIALMKLAGPTFTNEMIPVCLPNSSENFPGKVCWTSGWGTGDDGASPVLNAA 360  
QY 361 VPLISNKTICNRDYYVGGIISPSMLCAGYLTCGVDSQCGDGGPLVCOBERRLKLVGATSF 420  
DQ 361 VPLISNKTICNRDYYVGGIISPSMLCAGYLTCGVDSQCGDGGPLVCOBERRLKLVGATSF 420  
QY 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMRDLKT 453  
DQ 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMRDLKT 453

RESULT 3  
TMS2\_HUMAN  
ID TMS2\_HUMAN STANDARD; PRT; 492 AA.  
AC O15393; Q9BXX1;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Transmembrane protease, serine 2 precursor (EC 3.4.21.-).  
GN TMPRSS2 OR PRSS10.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97468144; PubMed=9325052;  
RA Paoloni-Giacobino A., Chen H., Peitsch M.C., Rossier C.,  
RA Antonarakis S.E.;  
RT "Cloning of the TMPRSS2 gene, which encodes a novel serine protease  
RT with transmembrane, LDLRA, and SRCR domains and maps to 21q22.3";  
RL Genomics 44:309-320 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21309069; PubMed=11414763;  
RA Teng D.H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.;  
RA "Mutation analyses of 268 candidate genes in human tumor cell lines";  
RL Genomics 74:352-364 (2001).  
RN [3]  
RP SEQUENCE FROM N.A. AND MUTAGENESIS.  
RX MEDLINE=21139112; PubMed=11245484;  
RA Afar D.E.H., Vivanco I., Hubert R.S., Kuo J., Chen E., Saffran D.C.,  
RA Raitano A.B., Jakobovits A.;  
RA "Catalytic cleavage of the androgen-regulated TMPRSS2 protease results  
RT in its secretion by prostate and prostate cancer epithelia";  
RL Cancer Res. 61:1686-1692 (2001).  
RN [4]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=21104370; PubMed=11169526;  
RA Vaarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihko P.T.;  
RA "Expression of transmembrane serine protease TMPRSS2 in mouse and  
RT human tissues";  
RL J. Pathol. 193:134-140 (2001).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Activated by  
CC cleavage and secreted.  
CC -1- TISSUE SPECIFICITY: Expressed strongly in small intestine. Also  
CC expressed in prostate, colon, stomach and salivary gland.  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.  
CC -1- SIMILARITY: Contains 1 SRCR domain.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL: U75329; AAC51784.1; -  
DR EMBL: AF123453; AAD37117.1; -  
DR EMBL: AF270487; AAK29280.1; -  
DR HSPF: P00783; IDPO.  
DR MEROPS: S01.247; -  
DR Genew: HGNC:11876; TMPRSS2.  
DR MIM: 602060; -  
DR GO: GO:005887; C: integral to plasma membrane; TAS.  
DR GO: GO:008236; F: serine-type peptidase activity; TAS.  
DR InterPro: IPR009003; Cys Ser trypsin.  
DR InterPro: IPR002172; LDL\_receptor\_A.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR InterPro: IPR001190; Srcr\_receptor.  
DR Pfam: PF0089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SM00192; LDLA; 1.  
DR SMART: SM00202; SR; 1.  
DR SMART: SM00202; tryp\_SPC; 1.  
DR PROSITE: PS01209; LDLRA\_1; 1.  
DR PROSITE: PS0068; LDLRA\_2; 1.  
DR PROSITE: PS00420; SRCR\_1; FALSE\_NEG.  
DR PROSITE: PS0287; SRCR\_2; 1.  
DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen;  
KW Polymorphism.  
FT CHAIN 1 255 TRANSMEMBRANE PROTEASE, SERINE 2, NON-  
FT CATALYTIC CHAIN. CATALYTIC CHAIN.  
FT CHAIN 256 492 TRANSMEMBRANE PROTEASE, SERINE 2,  
FT CATALYTIC CHAIN. CATALYTIC CHAIN.  
FT DOMAIN 1 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 85 105 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT (POTENTIAL).  
FT DOMAIN 106 492 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 112 149 LDL-RECEPTOR CLASS A.  
FT DOMAIN 150 242 SRCR.  
FT DOMAIN 256 492 SERINE PROTEASE.  
FT ACT\_SITE 296 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 345 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 441 441 CHARGE RELAY SYSTEM.  
FT SITE 255 256 CLEAVAGE (POTENTIAL).  
FT DISULFID 113 126 BY SIMILARITY.  
FT DISULFID 120 139 BY SIMILARITY.  
FT DISULFID 133 148 BY SIMILARITY.  
FT DISULFID 172 231 BY SIMILARITY.  
FT DISULFID 185 241 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 244 365 BY SIMILARITY.  
FT DISULFID 281 297 BY SIMILARITY.  
FT DISULFID 410 426 BY SIMILARITY.  
FT DISULFID 437 463 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 213 213 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 249 249 N-LINKED (GLCNAC... (POTENTIAL).  
FT VARIANT 449 449 K -> N (in dbSNP:1056602).  
FT MUTAGEN 255 255 R -> Q: LOSS OF CLEAVAGE.  
FT MUTAGEN 441 441 S -> A: LOSS OF ACTIVITY.  
FT CONFLICT 160 160 M -> V (IN REF. 3).  
FT CONFLICT 242 242 I -> L (IN REF. 1).  
FT CONFLICT 329 329 E -> Q (IN REF. 1).  
FT CONFLICT 489 491 RAD -> KAN (IN REF. 1).  
SQ SEQUENCE 492 AA; 53891 MW; CAB44FD1749076S CRC64;  
Query Match 36.1%; Score 882; DB 1; Length 492;  
Best Local Similarity 45.7%; Pred. No. 5.2e-67;  
Matches 188; Conservative 54; Mismatches 149; Indels 20; Gaps 10;





|   |   |  |                |                                     |    |  |
|---|---|--|----------------|-------------------------------------|----|--|
| FT  | DISULFID  | 76   | 125            | BY SIMILARITY.                      | RL | Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.                   |
| FT  | DISULFID  | 119  | 138            | BY SIMILARITY.                      | RP | [2]  |
| FT  | DISULFID  | 132  | 147            | BY SIMILARITY.                      | RC | SEQUENCE FROM N.A. (ISOFORM 4).  |
| FT  | DISULFID  | 171  | 230            | BY SIMILARITY.                      | RA | TISSUE=Brain;  |
| FT  | DISULFID  | 184  | 240            | BY SIMILARITY.                      | RM | Mitsui S., Yamaguchi N.;   |
| FT  | DISULFID  | 243  | 363            | INTERCHAIN (BY SIMILARITY).         | RL | "Molecular cloning of mouse type 4 spinesin.";                             |
| FT  | DISULFID  | 279  | 395            | BY SIMILARITY.                      | RT | Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.                   |
| FT  | DISULFID  | 293  | 395            | BY SIMILARITY.                      | CC | -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).            |
| FT  | DISULFID  | 408  | 424            | BY SIMILARITY.                      | CC | -1- ALTERNATIVE PRODUCTS:  |
| FT  | DISULFID  | 435  | 463            | BY SIMILARITY.                      | CC | Event=Alternative splicing; Named isoforms=4;                              |
| FT  | CARBOHYD  | 111  | 111            | N-LINKED (GLCNAC. . .) (POTENTIAL). | CC | Name=4;  |
| FT  | CARBOHYD  | 212  | 212            | N-LINKED (GLCNAC. . .) (POTENTIAL). | CC | Isoid=Q9ER04-1; Sequence=Displayed;  |
| FT  | CARBOHYD  | 474  | 474            | N-LINKED (GLCNAC. . .) (POTENTIAL). | CC | Name=1;  |
| FT  | CONFLICT  | 122  | 122            | S -> L (IN REF. 3).                 | CC | Isoid=Q9ER04-2; Sequence=VSP_005397, VSP_005398;                           |
| FT  | CONFLICT  | 178  | 178            | S -> H (IN REF. 1).                 | CC | Name=2;  |
| FT  | CONFLICT  | 320  | 320            | Y -> H (IN REF. 1).                 | CC | Isoid=Q9ER04-3; Sequence=VSP_005395;                                       |
| FT  | CONFLICT  | 474  | 474            | N -> D (IN REF. 1).                 | CC | Name=3;  |
| SQ  | SEQUENCE  | 490 AA; 53479 MW; 07D2B03EAD8A1A9 CRC64;                     |                |                                     | CC | Isoid=Q9ER04-4; Sequence=VSP_005396;                                       |
| Query Match   |   |  |                |                                     | CC | -1- SIMILARITY: Belongs to peptidase family S1.                            |
| Best Local Similarity 41.0%; Pred. No. 2e-66;                     |   |  |                |                                     | CC | -1- SIMILARITY: Contains 1 SRCR domain.                                    |
| Matches 193; Conservative 66; Mismatches 146; Indels 66; Gaps 13; |   |  |                |                                     | CC | -----  |
| QY  | 28  | EVAPDADAAQLSLPLKFFPIIV                                       | -----IGII----- | A 58                                | CC | This SWISS-PROT entry is copyright. It is produced through a collaboration |
| Db  | 31  | PVAPNG-----YNLYPAQYVPSVPQVAPRITTAQASTSVIHTPKSGAPCTSKSKS      | 83             |                                     | CC | between the Swiss Institute of Bioinformatics and the EMBL outstation -    |
| QY  | 59  | LILALAIGLGI-----HFDGS-GKIRCRSFKCIELIARCDGVSDCKGDG            | 103            |                                     | CC | the European Bioinformatics Institute. There are no restrictions on its    |
| Db  | 84  | LCIALALGTVLTGAAVAALLWRFWDSNCSGTEMECGSGTCTSSSLWCDGVAHCPNGED   | 143            |                                     | CC | use by non-profit institutions as long as its content is in no way         |
| QY  | 104   | EYRCVRVGGNAVLOVFTA--ASWTKMCDSDKNGHYANVACQLGPP-SYVSSDNLRVSS   | 160            |                                     | CC | modified and this statement is not removed. Usage by and for commercial    |
| Db  | 144   | ENRCVLYGQSFLOYSORKAWYPCQDDNSESIGRAACKDMGYKNFYSGQIPQDS        | 203            |                                     | CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |
| QY  | 161   | LEQCFREEFVSIDHLLPDKVTALHRSVYREGCASGHVTVLQCTACGHRH-GYSSRVIG   | 219            |                                     | CC | or send an email to license@isb-sib.ch).                                   |
| Db  | 204   | GATSFMKLVNSGNV---DLYKLIYHS-----DSCSRMVVSLRCEGVRSVKRQSRIVG    | 256            |                                     | CC | -----  |
| QY  | 220   | GNMSLLSQWPQASLOFQVHLGGSVITPLWITTAHCVYD-LYLPKSWITQVGLV--S     | 276            |                                     | CC | EMBL; AB016229; BAB20276.1; -  |
| Db  | 257   | GLNASPGDWQVSLVQGVHVGCGSIIPEWIVTAAHCVBEPPLSGFRYWTAFAGILRS     | 316            |                                     | CC | EMBL; AB016230; BAB20277.1; -  |
| QY  | 277   | LLDNPAHSLVKEIVVHSYKPKRLGNDIALMKLAGLPLFNMIOQVCLPNSEENFPDGG    | 336            |                                     | CC | EMBL; AB016423; BAB20278.1; -  |
| Db  | 317   | LMFY-GSRHQVEKVIHPNYDSKTNDIALMKLQTLPLFNDLVKPVCLPQGMWMLDLQ     | 375            |                                     | CC | EMBL; AB041037; BAB40328.1; -  |
| QY  | 337   | VCMTSGWATEDGDGASPVNLHAAVPLISNKI CNHRDVTGGIISPSMLCAGYLTGGVDSC | 396            |                                     | CC | HSP; P00763; IDPO.   |
| Db  | 376   | ECWISGWGATYKGTSDVLNAAMVPLIEPSKNSKIYNNLITPAMICAGFLQGSVDSC     | 435            |                                     | CC | MEROPS; S01313; -  |
| QY  | 397   | QGDSGGPLVCQERELMKLVGATSGFGICARVNPQGVVTRVTSFLDWIHEQM          | 447            |                                     | CC | InterPro; IPR003407; Tmpress5.   |
| Db  | 436   | QGDSGGPLVTLKNGIWLIGDTSGSCAKALRPQVGVNTVTDNIYQOM               | 486            |                                     | CC | InterPro; IPR009003; Cys_Ser trypsin.                                      |
| RESULT 5  |   |  |                |                                     | CC | InterPro; IPR001254; Peptidase S1.   |
| ID  | TMSS_MOUSE  | STANDARD;  | PRT;           | 455 AA.                             | CC | InterPro; IPR001314; Peptidase S1A.  |
| AC  | Q9ER04; Q9ER02; Q9ER03;   |  |                |                                     | CC | InterPro; IPR001190; Srcr_receptor.  |
| DT  | 16-OCT-2001 (Rel. 40, Created)                                      |  |                |                                     | CC | Pfam; PF00089; trypsin1.   |
| DT  | 16-OCT-2001 (Rel. 40, Last sequence update)                         |  |                |                                     | CC | PRINTS; PR00722; CHYMOTRYPSIN.   |
| DT  | 28-FEB-2003 (Rel. 41, Last annotation update)                       |  |                |                                     | CC | SMART; SMO0020; TRYPSIN_SPC; 1.  |
| DE  | Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).          |  |                |                                     | CC | PROSITE; PS00240; TRYPSIN_DOM; 1.  |
| GN  | TMPSR95.  |  |                |                                     | CC | PROSITE; PS00134; TRYPSIN_HIS; 1.  |
| OS  | Mus musculus (Mouse).   |  |                |                                     | CC | PROSITE; PS00135; TRYPSIN_SER; 1.  |
| OC  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |  |                |                                     | CC | PROSITE; PS00420; SRCR_1; FALSE_NEG.                                       |
| CC  | Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |  |                |                                     | CC | PROSITE; PS00287; SRCR_2; 1.   |
| OK  | NCBI_taxid=10090;   |  |                |                                     | CC | Hydrolase; Serine protease; Transmembrane; Signal-anchor;                  |
| FN  | [1]   |  |                |                                     | CC | Glycoprotein; Alternative splicing.  |
| RP  | TISSUE=Brain;   |  |                |                                     | CC | DOMAIN 1 49  |
| RC  | Mitsui S., Yamaguchi N.;  |  |                |                                     | CC | DOMAIN 50 70   |
| RA  | "cDNA cloning of mouse spinesin.";                                  |  |                |                                     | CC | TRANSMEM 1 49  |
| RT  |   |  |                |                                     | CC | DOMAIN 71 455  |
|   |   |  |                |                                     | CC | DOMAIN 112 207   |
|   |   |  |                |                                     | CC | DOMAIN 218 455   |
|   |   |  |                |                                     | CC | ACT SITE 258 308   |
|   |   |  |                |                                     | CC | ACT SITE 308 358   |
|   |   |  |                |                                     | CC | ACT SITE 405 405   |
|   |   |  |                |                                     | CC | SITE 217 218   |
|   |   |  |                |                                     | CC | DISULFID 135 196   |
|   |   |  |                |                                     | CC | DISULFID 148 206   |
|   |   |  |                |                                     | CC | DISULFID 209 328   |
|   |   |  |                |                                     | CC | DISULFID 243 259   |
|   |   |  |                |                                     | CC | DISULFID 374 390   |
|   |   |  |                |                                     | CC | DISULFID 401 429   |
|   |   |  |                |                                     | CC | CARBOHYD 163 163   |
|   |   |  |                |                                     | CC | CARBOHYD 170 170   |
|   |   |  |                |                                     | CC | CARBOHYD 319 319   |
|   |   |  |                |                                     | CC | CARBOHYD 375 375   |
|   |   |  |                |                                     | CC | VARSPLIC 1 144   |
|   |   |  |                |                                     | CC | VARSPLIC 1 10  |

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FT VARSPLIC 1 182 /FTID=VSP 005396.
FT Missing (in isoform 1).
FT FTID=VSP 005397.
FT VARSPLIC 183 192 GGLVEEAWKP -> MEAQVGLLMV (in isoform 1).
FT FTID=VSP 005398.
FT CONFLICT 325 325 D -> G (IN REF. 1; BAB202777).
FT SEQUENCE 455 AA; 49632 MW; 5CF31789C6899AA CRC64;

Query Match 28.5%; Score 695.5; DB 1; Length 455;
Best Local Similarity 35.1%; Pred. No. 2.9e-51;
Matches 150; Conservative 63; Mismatches 161; Indels 53; Gaps 12;

QY 52 IVIGIALLALAIG---LGIHFDGSGKYRCSSPKFCELIARCDGVSCKDGEDEYR-- 106
DB 50 VILGVLLGAGIAGIASHLLVILWPAASPSISGTLQEEWTLNCPGVS-C---EEELPS 105
QY 107 -----CVRGGQNAVLOVFTAA--SWKTCMSDDWKGHYANVACAQIGPPSVSSDNLVRS 159
DB 106 LPKTVSFRINGEDLLQVQVREARPDWLLVCHEGWSPALGMHCKSLGHIRLTQHKAVALS 165
QY 160 SLEGGQREEFVSIDHLLPDDKVTALHSHVYVREG-----CASGHVVTLOCTAC 207
DB 166 DIKINSQFAQLS-----ARPGGLVEEAWKPSANCPGSRIVSLKSEC 209
QY 208 GHRGYSRIVGNGMSSLQWPMQASLQFGYHLCGGSVITPLWITAAHCYVDLYLPK- 266
DB 210 G-ARPLASRIVGGQAVASGRWPQASVWLGRHTCGASVLAPHVWVTAACHMYSFRLSRL 268
QY 267 -SWTIQVGLVLLDNPAPSH--LVKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMQ 322
DB 269 SSWRVHAGLVLS--HGAVROHQGTWVEKILPHPLYSACNHDYDVALLOLRTPINFSDTVA 326
QY 323 VCLPNSEENFPDGKVCWTSGWATEDG-GDASPLNHAAPVLTISNKCINHRDVGIIISP 381
DB 327 VCLPAKEQYEPWGSQCWVSGWHTDSHTSHSDTLQDTWVLLSTHLNCSWCYSGALTH 386
QY 382 SMLCAGVLTGVDSQCGSGGLPVCOERLKLKLVGATSGFGICAEVKNKGVTYRTVSFLD 441
DB 387 RMLCAGYLDGRADACQDGSGLPLVCPGSDTWHLVGVVSGRGCAEPNREGVAKVAEFLD 446
QY 442 WIHEOME 448
DB 447 WIHDTVQ 453

RESULT 6
TMS5 HUMAN STANDARD; PRT; 457 AA.
AC Q9H33;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN TWPRSS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX PubMed=11741986;
RA Yanaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;
RT "Spinesin/TWPRSS5, a novel transmembrane serine protease, cloned from
human spinal cord.";
RL J. Biol. Chem. 277:6806-6812(2002).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in
neurons, in their axons, and at the synapses of motoneurons in the
spinal cord.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 SRCR domain.

```

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CC or send an email to license@isb-sib.ch).
CC -----
DB EXBL; AB028140; BAB20375.1; -.
DR HSP; P00763; IDPO.
DR Genew; HGNC:14908; TWPRSS5.
DR MIM; 606751; -.
DR MEROPS; S01.313; -.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00089; tryptsin; .
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS0289; SRCR_2; FALSE_NEG.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW Glycoprotein.
FT DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 71 457 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 112 207 SRCR.
FT DOMAIN 218 457 SERINE PROTEASE.
FT ACT_SITE 258 258 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 308 308 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 405 405 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE 217 218 CLEAVAGE (POTENTIAL).
FT DISULFID 135 196 BY SIMILARITY.
FT DISULFID 148 206 BY SIMILARITY.
FT DISULFID 209 328 BY SIMILARITY.
FT DISULFID 243 259 BY SIMILARITY.
FT DISULFID 374 390 BY SIMILARITY.
FT DISULFID 401 429 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 457 AA; 49574 MW; 64406AB4985A2651 CRC64;

Query Match 28.2%; Score 689.5; DB 1; Length 457;
Best Local Similarity 35.2%; Pred. No. 9.4e-51;
Matches 149; Conservative 58; Mismatches 175; Indels 41; Gaps 8;

QY 53 VIGIALLALAIGLGHFDGSGKYRCSSPKFCELIARCDGVSCKDGEDEYRCVRVG 112
DB 51 VILGALLAGVGSWLLV---LYLCPAASQPSIS-----GTLQDEBITLSCSEASA 98
QY 113 QNAVL-----QVETAASWTKMCSDDWKGHYANVACAQIGPPSVS 152
DB 99 EEALLPALPKTVSFRINSEDFLLERQVRDQRPWLLVCHEGWSPALGLQICWSLGHRLTH 158
QY 153 SDNLVRSLEGGQREEFVSIDHLLPDDKVTALHSHVYVREGCASGHVVTLOCTACGHR 212
DB 159 HKGVNLTIDKLNSSQFAQLSPRLGG---FLEEAWQPRNNCTSGQVSLRSCSEG-ARP 213
QY 213 YSRIVGNGMSSLQWPMQASLQFGYHLCGGSVITPLWITAAHCYVDLYLPK--SWT 270
DB 214 LASRIVGSGQVAPGWPQASVALGFRHTCGSVLAPRWVVTAAACHMHSFRLARLSWRV 273
QY 271 QVGLYS-LILDNPAPSHLVEKIVHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSE 329
DB 274 HAGLVSHSAVRPHQALVERIIPHPLYSAQNHDYDVALLOLRTPINFSDTGVACVLPKE 333

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QY 378 IISPSMLCAGYLGTGVDSCGGSGGGLVQCBRLWLKVGATSGFGICARVWKPQVYTRVT 437  
 Db 363 EVFAEMLCAGTPOGGKDTCCGSGGGLVWTHSK-NQVVGIVSWGRCGGSPFGYTKVT 421

QY 438 SFLDTHIEQMERDL 451  
 Db 422 AVLNWYVNRKSEM 435

## RESULT 8

HEPS\_HUMAN STANDARD; PRT; 417 AA.  
 AC PS5981;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine 1).  
 DE 1).  
 OS Homo sapiens (Human).  
 GN HPN OR TMPRSS1.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88209431; PubMed=2835076;  
 RA Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;  
 RT "A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain expressed by human liver and hepatoma cells.";  
 RL Biochemistry 27:1067-1074(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas, and Spleen;  
 RX MEDLINE=23388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=91358502; PubMed=1885621;  
 RA Teuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S., Chou S.H., Kurachi K.;  
 RT "Hepsin, a cell membrane-associated protease. Characterization, tissue distribution, and gene localization.";  
 RL J. Biol. Chem. 266:16948-16953(1991).  
 RN [4]  
 RP CHARACTERIZATION  
 RX MEDLINE=93348237; PubMed=8346233;  
 RA Torres-Rosado A., O'Shea K.S., Teuji A., Chou S.H., Kurachi K.;  
 RT "Hepsin, a putative cell-surface serine protease, is required for mammalian cell growth.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).  
 CC -!- FUNCTION: Plays an essential role in cell growth and maintenance of cell morphology.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -!- TISSUE SPECIFICITY: Present in most tissues, with the highest level in liver.  
 CC -!- SIMILARITY: Belongs to peptidase family S1.  
 CC  
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CC EMBL; M18930; AAA36013.1; -  
 DR EMBL; X07732; CAA30558.1; -  
 DR EMBL; X07002; CAA30058.1; -  
 DR EMBL; BC025716; AAH25716.1; -  
 DR PIR; S00845; S00845.  
 DR HSP; P00763; LDPO.  
 DR MEROPS; S01.224; -  
 DR Genew; HGNC:5155; HFN.  
 DR MIM; 142440; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.  
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease; Transmembrane; Signal-anchor.  
 FT CHAIN 1 162  
 FT SERINE PROTEASE HEPsin, NON-CATALYTIC CHAIN (POTENTIAL).  
 FT SERINE PROTEASE HEPsin, CATALYTIC CHAIN (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT SERINE PROTEASE.  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT INTERCHAIN (BY SIMILARITY).  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT B2086FF661E551D7 CRC64;  
 SQ SEQUENCE 417 AA; 45011 MW; B2086FF661E551D7 CRC64;

Query Match 27.6%; Score 674; DB 1; Length 417;  
 Best Local Similarity 35.8%; Pred. No. 1.7e-49;  
 Matches 149; Conservative 62; Mismatches 143; Indels 62; Gaps 11;  
 QY 59 LILALAIGLTHFDGSGYKRCRSFKICELIARCDGVSDCKDGEYRCVVGQNAVQLQ 118  
 Db 26 LLLLTALG-----AASWAIWVLRSD-----QELYPVQVSSADARLM 64  
 QY 119 VF--TAASWKTCSDNDKGVHANYACQAGLPFSVSDNLNVSLVSGLEQGFREFFVSDHLL 176  
 Db 65 VFDKTEGTWRLICSSRSRNARVAGLSCEMGFLRALTHTSELDVRTAGANGTSGFCVDE-- 122  
 QY 177 PDDKVTALHSHVYVRE-----GCASGHVVTIQCACGHRGYSRSIRVGGNNLSLSQWPQ 231  
 Db 123 -----GRLPQRLLEVTSVCCDPRGFLAICQDGRKLPVDRIVGGRTSLGRFPWQ 177  
 QY 232 ASLPQGGYHLCGGSVITPLWITTAHCYVDLYLPK-----SWTIQGLVSLLLNPNAPSH 285  
 Db 178 VSLRYDGAHLCCGSLSGDWLTAHC-----FPERNRVLSRWVFAVAVA---QASPHG 229



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FT DISULFID 206 225 BY SIMILARITY.
FT DISULFID 219 236 BY SIMILARITY.
FT DISULFID 659 671 BY SIMILARITY.
FT DISULFID 666 684 BY SIMILARITY.
FT DISULFID 678 693 BY SIMILARITY.
FT DISULFID 788 912 INTERCHAIN (BY SIMILARITY).
FT DISULFID 826 842 BY SIMILARITY.
FT DISULFID 928 933 BY SIMILARITY.
FT DISULFID 957 972 BY SIMILARITY.
FT DISULFID 983 1011 BY SIMILARITY.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 264 264 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 486 486 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 550 550 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 722 722 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 741 741 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 762 762 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 864 864 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 903 903 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 965 965 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 166 192 Missing (in isoform Short).
FT CONFLICT 808 808 R -> Y (IN REF. 3).
FT SEQUENCE 1035 AA; 114887 MW; E207970308296E13 CRC64;

Query Match 27.4%; Score 669.5; DB 1; Length 1035;
Best Local Similarity 37.0%; Pred. NO. 1.2e-48;
Matches 146; Conservative 70; Mismatches 146; Indels 33; Gaps 14;

QY 66 GLGIHFDG-SGKYCRSPFKTEIARCDGVSDCKDGEYRCVRV---GGONAVLOVF 120
DB 652 GLGIPECKEDNFQCKDG-ECIPLVNLCDGFPCDKGSDAHCVALFNGTTDSSGLGVQFR 710
QY 121 TAASWTMCSDDKHGHYANVACQGLFPYSVDNLRVSSLSGQFRBEFVSTIDHLLPDK 180
DB 711 IQSINHWACAEANNWTTQISDDVCQLLGLGT--GNSSVPTFTSGG---GPVYNLN----- 758
QY 181 VTALHHSVYV--REGCASGHVTLQCT--ACGHR---RGYSRIYGVGNMILLSQMPQAS 233
DB 759 -TAPNGSLITSPQCLESLILLQCNYSCKGLVTQEVSPKIVGSDSRREGANPWVVA 817
QY 234 LOPQGYHLCGGSVITPLWITAAHCYVDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEK 289
DB 818 LYPDDQVCGASLVSRLDLSAARHCYVGRNMFPSKKAIVGLHMASNLTSPOIETRLIDQ 877
QY 290 IYVHSKYKPKLGNLDIALMKLAGLPTFNEMIQVCLPNSSENFPPDKVCTWTSNGATGD 349
DB 878 IVINPHYNKRRKNDIAMHLEMKVNTYDIQIFCLPEENQVFPFPGRICSIAGWALLIYQ 937
QY 350 GDASPVLNHAAPLISNKICNHR-DVYGGIISPSMLCAGYLTGVDSCQDSCGSGPLVCQE 408
DB 938 GSTADVLQEAADVLLSNEXCQQQOMPEYN--ITENMVACGYAGGVDSQDSCGSGPLMCQE 995
QY 409 RRLWKLVGATSPGICGAENVKPOVYTRVTSFLDWI 443
DB 996 NNRWLLAGVTSFGYQCALPNRPGVARYVPRFTEWI 1030

RESULT 10
ENTK_HUMAN
ID_ENTK_HUMAN STANDARD; PRT; 1019 AA.
AC_P98073;
DT 01-FEB-1996 (Rel. 33, Created)

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).
GN PRSS7 OR ENTK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ductenium;
RX MEDLINE=95234679; PubMed=7718557;
RA Kitamoto Y., Veile R.A., Denis-Keller H., Sadler J.E.;
RT "cDNA sequence and chromosomal localization of human enterokinase,
RL the proteolytic activator of trypsinogen.";
RN [2]
RP SEQUENCE FROM N.A., AND DISEASE.
RX MEDLINE=21606074; PubMed=11719902;
RA Holzinger A., Maier E.M., Buck K., Mayerhofer P.U., Kappler M.,
RX Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher A.A.;
RA "Mutations in the proenteropeptidase gene are the molecular cause of
RT congenital enteropeptidase deficiency.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20299799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Faudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordisiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehrmeyer S., Borzmy K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [4]
RP SEQUENCE OF 749-1019 FROM N.A.
RC TISSUE=Ductenium;
RX MEDLINE=94329561; PubMed=8052624;
RA Kitamoto Y., Yuan Q., Wu Q., McCourt D.W., Sadler J.E.;
RT "Enterokinase, the initiator of intestinal digestion, is a mosaic
RL protease composed of a distinctive assortment of domains.";
CC Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
CC -!- FUNCTION: Responsible for initiating activation of pancreatic
CC proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC A). It catalyzes the conversion of trypsinogen to trypsin which in
CC turn activates other proenzymes including chymotrypsinogen,
CC procarboxypeptidases, and proelastases.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC trypsinogen.
CC -!- SUBUNIT: Heterodimer of a catalytic (light) chain and a
CC multidomain (heavy) chain linked by a disulfide bond.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Intestinal brush border.
CC -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC -!- DISEASE: Defects in PRSS7 are a cause of enterokinase deficiency
CC [MIM:226200]; a life-threatening intestinal malabsorption disorder
CC characterized by diarrhea and failure to thrive.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC -----
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Db      865 NPHYRRKNDNDIAMHLEFKVNYTDYTOPICLPEENVQFPGRNCISAGMTGVVYQTT 924
Qy      353 SPVLNHAAPVLIISKNICNHR-DVYGGIISPSMLCAGYLTGGVDSQGGSGGLVQCERRL 411
Db      925 ANILQADVPLLSNRCQQQMPYFN--ITENICAGYEKGIDSCQGGSGGLVQCENNR 982
Qy      412 WKLVGATSGICCAEVNKGVTGVTTSFLDWI 443
Db      983 WFLAGVTSFGYKCALFNPGVYARVSRFTWI 1014

RESULT 11
ENTK_PIG STANDARD; PRT; 1034 AA.
AC P98074;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).
GN PRS7 OR ENTK
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Ductal mucosa;
RX MEDLINE=94327548; PubMed=8051081;
RA Matsushima M., Ichinose M., Yahagi N., Kakei N., Tsukada S.,
RA Miki K., Kurokawa K., Tashiro K., Shiohara K., Shinomiya K.,
RA Uemeyama H., Inoue H., Takahashi T., Takahashi K.;
RT "Structural characterization of porcine enteropeptidase.";
RL J. Biol. Chem. 269:19976-19982(1994).
CC -!- FUNCTION: Responsible for initiating activation of pancreatic
CC proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC A). It catalyzes the conversion of trypsinogen to trypsin which in
CC turn activates other proenzymes including chymotrypsinogen,
CC procarboxypeptidases, and proelastases.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC trypsinogen.
CC -!- SUBUNIT: Heterotrimer of a catalytic (light) chain, a multidomain
CC (heavy) chain, and a mini chain.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC -!- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC -----
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CC -----
DR EMBL; D30799; BAA06459.1; -;
DR HSP; P00763; IDPO.
DR MEROPS; S01.156; -.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001344; Peptidase_S1A.
DR InterPro; IPR000082; SEA_domain.
DR InterPro; IPR001190; Srcr_receptor.

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Pfam; PF00431; CUB; 2.
Pfam; PF00057; ldl_recept_a; 2.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF01390; SEA; 1.
DR Pfam; PF00530; SRCR; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00192; LDLa; 2.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00200; SEA; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; TYD_SPC; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01209; LDLRA_1; 2.
DR PROSITE; PS00668; LDLRA_2; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00660; MAM_2; 1.
DR PROSITE; PS00024; SEA; 1.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS00287; SRCR_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;
KW Zymogen; Transmembrane; Repeat; Lipoprotein.
FT CHAIN 52 117
FT CHAIN 118 799
FT CHAIN 800 1034
FT DOMAIN 1 18
FT TRANSMEM 19 47
FT DOMAIN 48 1034
FT DOMAIN 52 169
FT DOMAIN 197 238
FT DOMAIN 240 349
FT DOMAIN 357 519
FT DOMAIN 539 649
FT DOMAIN 656 694
FT DOMAIN 693 786
FT DOMAIN 800 1034
FT ACT_SITE 840 840
FT ACT_SITE 891 891
FT ACT_SITE 986 986
FT LIPID 2 2
FT DISULFID 199 212
FT DISULFID 206 225
FT DISULFID 219 236
FT DISULFID 658 670
FT DISULFID 665 683
FT DISULFID 677 692
FT DISULFID 787 911
FT DISULFID 825 841
FT DISULFID 925 992
FT DISULFID 956 971
FT DISULFID 982 1010
FT CARBOHYD 116 116
FT CARBOHYD 147 147
FT CARBOHYD 170 170
FT CARBOHYD 194 194
FT CARBOHYD 283 283
FT CARBOHYD 343 343
FT CARBOHYD 350 350
FT CARBOHYD 403 403
FT CARBOHYD 455 455
FT CARBOHYD 485 485
FT CARBOHYD 518 518
FT CARBOHYD 549 549
FT CARBOHYD 645 645
FT CARBOHYD 697 697
FT CARBOHYD 701 701

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FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 863 863 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 902 902 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1034 AA; 114776 MW; 0388C64CF64C368 CRC64;

Query Match 27.2%; Pred. No. 3.9e-48; Length 1034;
Best Local Similarity 37.8%;
Matches 149; Conservative 65; Mismatches 147; Indels 33; Gaps 14;

QY 67 LGIHFDG-SGKYRCSRFKIELIARCGVSGCKDGEDYRCVR-----VGQNAVLFQVET 121
Db 652 LGIPBCKEDNFQCENG-ECVLVNLCDGFSCHKDGSDEAHCVRFLNGTANNGLVQPRI 710
QY 122 AASWKTMSDDNKGHYANVACAQLGFPFVSVDNLSVSLGQFREFVSVSDHLLPDDKV 181
Db 711 QSIWHTACAEWNTQTSDVDCVLLGLGTGNSMPF-FSSGGG-----PFVKLN----- 757
QY 182 TALHSHVYV--REGCASGHVVTIQT--ACGHR--RGYSSRIVGNGMSSLISQWFWQASL 234
Db 758 TAPNGSLILTASGQCFEDSLILQCNHSCGKKQVAQEVSPKIVGNDREGAMPVVAL 817
QY 235 QFGYHLCGSGVITPWIITAHCVTDLYL-PKSWTIQVGL--VSLDNP-APSHLVEKI 290
Db 818 YNGQLLCGASVSRDVLWSAAHCYVGRNLEPSKWKAILGLHMTNLTSPQIVTFLIDEI 877
QY 291 VHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSBENFPDGKVCVTSWGATEDGG 350
Db 878 VINPHYNRRKDSDIAMHLEFKVYTDYIQCIPLEENQVPPGRCISGACWGVYQG 937
QY 351 DASPVLNHAAPVLSIKNIENR-DVTGGIISPSMLCAGYLTGVDSQCDGSGPLVCQER 409
Db 938 SPADIIQEAADVPLLSNEKQQQMPYEN--ITENMCAGYEBGIDSCQDGSGLPLMCLEN 995
QY 410 RLKMLVGATSGFGICAEVKNKPGVYTVTGTFLDWI 443
Db 996 NRLLAGVTSFGYQCALNRPGRYANVPKTEWI 1029

RESULT 12
HEPS_MOUSE
ID _HEPS_MOUSE STANDARD; PRT; 436 AA.
AC Q35453; Q9C9W7;
DT 15-JUL-1998 (Rel. 36, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Serine protease hepsin (EC 3.4.21.-).
GN HPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Liver;
RX MEDLINE=98058912; PubMed=9395459;
RA Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.;
RT "Identification and cloning of the membrane-associated serine
protease, hepsin, from mouse preimplantation embryos.";
RL J. Biol. Chem. 272:31315-31320(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=99339944; PubMed=10411637;
RA Kawamura S., Kurachi S., Devashiki Y., Kurachi K.;
RT "Complete nucleotide sequence, origin of isoform and functional
characterization of the mouse hepsin gene.";
RL Eur. J. Biochem. 262:755-764(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX STRAIN=C57BL/6J; TISSUE=Kidney;

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caavaant T.,
RA Fleischmann W., Gaasterland Y., Glasi C., King B., Koshiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schram L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Scorch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayaishizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
CC -!- FUNCTION: Plays an essential role in cell growth and maintenance
of cell morphology.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=1a; Sequence=Displayed;
IsoId=O35453-1;
Note=Minor isoform;
Name=2; Synonyms=2a;
IsoId=O35453-2; Sequence=VSP_007232;
Note=Major isoform;
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to
frameshifts in positions 155, 191 and 233.
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-----
EMBL; AF030065; AAB84221.1;
EMBL; AK002694; BAB22289.2; ALT_FRAME.
DR HSP; P00763; IDPO.
DR MESOP; S01-224; -.
DR MGP; MGI:1196620; Hpn.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00202; SR; 1.
DR SMART; SM00202; TRYP-SPC; 1.
DR PROSITE; PS00240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW Alternative splicing.
FT CHAIN 1 181
SERINE PROTEASE HEPsin, NON-CATALYTIC
CHAIN (POTENTIAL).
FT CHAIN 182 436
SERINE PROTEASE HEPsin, CATALYTIC CHAIN
(POTENTIAL).
FT DOMAIN 21 36
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 63
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 64 436
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 182 436
SERINE PROTEASE.
FT ACT_SITE 222 222
CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 276 276
CHARGE RELAY SYSTEM (BY SIMILARITY).

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FT ACT_SITE 372 372 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 172 296 INTERCHAIN (BY SIMILARITY).
FT DISULFID 207 223 BY SIMILARITY.
FT DISULFID 341 357 BY SIMILARITY.
FT DISULFID 368 400 BY SIMILARITY.
FT CARBOHYD 131 131 Missing (in isoform 2).
FT VARSPLIC 25 44 /FTIdVSP 007232.
FT CONFLICT 85 85 L -> F (IN REF. 2 AND 3).
FT CONFLICT 204 204 T -> Y (IN REF. 3).
FT CONFLICT 214 214 G -> R (IN REF. 3).
FT CONFLICT 228 229 NR -> ET (IN REF. 3).
FT CONFLICT 264 264 P -> L (IN REF. 3).
FT CONFLICT 281 281 H -> N (IN REF. 3).
SQ SEQUENCE 436 AA; 46787 MW; 4A0993148C620BD0 CRC64;

Query Match 27.0%; Score 659.5; DB 1; Length 436;
Best Local Similarity 38.6%; Pred. No. 3.1e-48;
Matches 136; Conservative 49; Mismatches 128; Indels 39; Gaps 7;

QY 121 TAASWTKMCDSDWKGHYANVACAQLQPPSVSSDNLRVSLGQFREFEFVSID-----173
Db 88 TEGTWLLCKSSRNARVAGLCGEMGLRALAHSELDVTRAGANGTSFGFCVDEGGLPLA 147
QY 174 -HLPPDKVTALHSHVYVREGCGASHVVTLOCTACHRRGYSRIYVGNMILLSQWPQQA 232
Db 148 QRLT--DVISVC-----DCPRGRLTATCQDCGRRLPLVDRIYVGGQSSLRWPQV 197
QY 233 SLQFQGHLCGGSVITPLWITTAHCVYDYLK-----SWIQGLVSLDNPAPSHL 286
Db 198 SLRDGTHLCGSLSDGWVITAHG-----FFERNVLSRWVAFAGVARTSPHAVQLG 252
QY 287 VEKIVYHSKYKPK-----LGNDIALMKLAGLTFNEMIQVCLPNSENFDPGKVCWT 340
Db 253 VQAVIYHGGVLPFRDPTIDENSNDIALVHLSSLPLETEYIQVCLPAAGQALVDGKVT 312
QY 341 SGWATGDDGASVYLNHAAVPLSNKINHRDVGGLISPSVLCAGYLTGGVDSGCGS 400
Db 313 TSWGNTQFYQQAVLQEARVPLISNEVCNPFYGNQIRKPMFCAGYPEGGIDACQGS 372
QY 401 GGPLVQCE---RLWLKLVGATSGIGCAEVNKGVTYRTVTSFLDITHEQME 448
Db 373 GGPFVCEDSIGTSRWRLCGIVSWGTCALARKEGVYTKVDFREMFIAIK 424

RESULT 13
TMS4 HUMAN
ID TMS4 HUMAN STANDARD; PRT; 437 AA.
AC QNRS4; QNRS4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine
DE protease 2) (MT-SP2).
GN TMRSS4 OR TMRSS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancratic carcinoma;
RX MEDLINE=20283276; PubMed=10825129;
RA Wallrapp C., Haenel S., Mueller-Pillasch F., Burchardt B.,
RA Iwamura T., Ruthenburger M., Lerch M.M., Adler G., Gress T.M.;
RT "A novel transmembrane serine protease (TMRSS3) overexpressed in
RT pancreatic cancer.";
RL Cancer Res. 60:2602-2606(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.;
RT "Mt-SP2, a novel type II membrane serine protease expressed in
RT trachea, colon, and small intestine: identification, cloning, and
```

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RT chromosomal localization.";
RL Submitted (DSC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Mazra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Probable protease. Seems to be capable of activating
CC ENAC (By similarity).
CC -!- SURCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: High levels in pancreatic, gastric, colorectal
CC and ampullary cancer. Very weak expression in normal
CC gastrointestinal and urogenital tract.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC -----
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CC -----
DR EMBL; AF179224; AAF74526.1; -
DR EMBL; AF216312; AAF31436.1; -
DR EMBL; BC011703; AAH1703.1; -
DR HSSP; P00763; LDPO.
DR MEROPS; S01.034; -.
DR GENE; HGNC:11878; TMRSS4.
DR MIM; 606565; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004252; P:serine-type endopeptidase activity; NAS.
DR GO; GO:0008508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLA; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01209; LDLA_1; FALSE_NEG.
DR PROSITE; PS00868; LDLA_2; FALSE_NEG.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS0287; SRCR_2; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS0134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
DR Hydrolase; Serine protease; Transmembrane; Signal-anchor.
KW
```

|   |   |   |                                     |  |     |
|---|---|---|-------------------------------------|--|-----|
| FT  | DOMAIN  | 1   | 32                                  | CYTOPLASMIC (POTENTIAL).   |     |
| FT  | TRANSMEM  | 33  | 53                                  | SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).            |     |
| FT  | DOMAIN  | 54  | 437                                 | EXTRACELLULAR (POTENTIAL).                                       |     |
| FT  | DOMAIN  | 61  | 93                                  | LDL-RECEPTOR CLASS A.  |     |
| FT  | DOMAIN  | 94  | 204                                 | SCR.   |     |
| FT  | DOMAIN  | 205   | 437                                 | SERINE PROTEASE.   |     |
| FT  | ACT_SITE  | 245   | 245                                 | CHARGE RELAY SYSTEM (BY SIMILARITY).                             |     |
| FT  | ACT_SITE  | 290   | 290                                 | CHARGE RELAY SYSTEM (BY SIMILARITY).                             |     |
| FT  | ACT_SITE  | 387   | 387                                 | CHARGE RELAY SYSTEM (BY SIMILARITY).                             |     |
| FT  | SITE  | 204   | 205                                 | CLEAVAGE (POTENTIAL).  |     |
| FT  | DISULFID  | 64  | 83                                  | BY SIMILARITY.   |     |
| FT  | DISULFID  | 77  | 92                                  | BY SIMILARITY.   |     |
| FT  | DISULFID  | 127   | 183                                 | BY SIMILARITY.   |     |
| FT  | DISULFID  | 140   | 193                                 | BY SIMILARITY.   |     |
| FT  | DISULFID  | 196   | 310                                 | BY SIMILARITY.   |     |
| FT  | DISULFID  | 230   | 246                                 | BY SIMILARITY.   |     |
| FT  | DISULFID  | 356   | 372                                 | BY SIMILARITY.   |     |
| FT  | DISULFID  | 383   | 410                                 | BY SIMILARITY.   |     |
| FT  | CARBOHYD  | 130   | 130                                 | N-LINKED (GLCNAC. . .) (POTENTIAL).                              |     |
| FT  | CARBOHYD  | 178   | 178                                 | N-LINKED (GLCNAC. . .) (POTENTIAL).                              |     |
| FT  | CONFLICT  | 1   | 31                                  | MLQDPDQPLNSLDVLPKPKRIPMETTRK -> MSNPCHA NPVSPWRPSES (IN REF. 2). |     |
| FT  | SEQUENCE  | 437 AA;   | 48204 MW;                           | 351B2FD4A8657B12 CRC64;  |     |
| Query Match   |   |   |                                     |  |     |
| Best Local Similarity 26.9%; Score 658; DB 1; Length 437;         |   |   |                                     |  |     |
| Matches 158; Conservative 75; Mismatches 146; Indels 64; Gaps 18; |   |   |                                     |  |     |
| QY  | 44  | LPLKFPPIIVIGIIALLA  | -----IGLGHFDCSGKYCRSFKC---IELIAR--- | 91   |     |
| DB  | 24  | IPMETRKVGIPIIALLSLAIIIVVLKIVLD---KV----                     | YFLCQQLHFIPRKQL                     | 76   |     |
| QY  | 92  | CDGVSCCKGDEYRC  | -----VRVGQNAVLOVPTAA--SWKTMSDDWKHYA | 138  |     |
| DB  | 77  | CDGELDCPLGEDBEHCKVSPPEGPAVAVRLSKDRSLQVLDSATGNWFSACFDNPT     | EAL                                 | 136  |     |
| QY  | 139   | NVACAQLGFPYVSSDNLRVSSLEGOFREBFVSDHLLPDDKVTALHSHVYVREG---    | CA                                  | 195  |     |
| DB  | 137   | ETACRQMGYS  | -----KPTFRAVEIGPDQDLVDVEITENSQELMRN | SSGPC  | 184 |
| QY  | 196   | SGHVVTLOCTACHRRGYSSRIVGGNMLLSQFWQASLOFGYHL                  | CGSVITPLMI                          | 255  |     |
| DB  | 185   | SGSLVSLHCLACG-KSLKTPRVVGGEEASVDSFPWQVSIQYDQKHVCGG           | SILDPHWLVA                          | 243  |     |
| QY  | 256   | AHCV---YDLVLPKSWTIQVGLVSLDNPAPSHLVEKIV---VHSKYKPKRLGNDIALMK | 309                                 |  |     |
| DB  | 244   | AHCPRKHTDYP---NWKVRAGSKL--GSFPLAVAKIIIEFNPMY-PK--DNDIALMK   | 295                                 |  |     |
| QY  | 310   | LAGEPLTNEMIQVCLPNSSENPFDGKVCWTSWGAT-EDGSDASPVLNHAAVPLISNKI  | 368                                 |  |     |
| DB  | 296   | LQPELTSGTVRPICLPFPDEELTPATPLIIGWFTKQNGKGVSDILLQASVQVIDSTR   | 355                                 |  |     |
| QY  | 369   | CNHRDVTGGIISPSMLCAGYLTGVDSQCGSGPLVCQERLKLVGATSF             | FGICAEVN                            | 428  |     |
| DB  | 356   | CNADDAVQGEVTEKMKCAGIPEGGVDTCCQDSGGPLMYQSDQ-WHVVGIVSWG       | YCGGPS                              | 414  |     |
| QY  | 429   | KPGVYTVTSFLDWIHEQMERDL                                      | 451                                 |  |     |
| DB  | 415   | TPGVYTKVSAYLNINYNVWKAEL                                     | 437                                 |  |     |
| RESULT 14   |   |   |                                     |  |     |
| HEPS_RAT  |   |   |                                     |  |     |
| ID  | HEPS_RAT  | STANDARD;   | PRT;                                | 416 AA.  |     |
| AC  | Q05511;   |   |                                     |  |     |
| DT  | 01-FEB-1994   | (Rel. 28, Created)  |                                     |  |     |
| DT  | 01-FEB-1994   | (Rel. 28, Last sequence update)                             |                                     |  |     |
| DT  | 10-OCT-2003   | (Rel. 42, Last annotation update)                           |                                     |  |     |
| DE  | Serine protease hepsin (EC 3.4.21.-).                             |   |                                     |  |     |
| GN  | HPN.  |   |                                     |  |     |
| OS  | Rattus norvegicus (Rat).  |   |                                     |  |     |
| OC  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |   |                                     |  |     |

|   |  |   |     |  |
|---|--|---|-----|--|
| OC  | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  |   |     |  |
| OX  | NCBI_TaxID=101116;   |   |     |  |
| RN  | [1]  |   |     |  |
| RP  | SEQUENCE FROM N.A.   |   |     |  |
| RC  | TISSUE=Liver;  |   |     |  |
| RX  | MEDLINE=93305733; PubMed=8318546;  |   |     |  |
| RA  | Farley D., Raymond F., Nick H.;  |   |     |  |
| RT  | "Cloning and sequence analysis of rat hepsin, a cell surface serine  |   |     |  |
| RL  | proteinase.";  |   |     |  |
| RRL   | Biochim. Biophys. Acta 1173:350-352(1993).   |   |     |  |
| CC  | !- FUNCTION: Plays an essential role in cell growth and maintenance  |   |     |  |
| CC  | of cell morphology.  |   |     |  |
| CC  | !- SUBCELLULAR LOCATION: Type II membrane protein.   |   |     |  |
| CC  | !- SIMILARITY: Belongs to peptidase family 51.   |   |     |  |
| CC  | -----  |   |     |  |
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| CC  | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |   |     |  |
| CC  | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |   |     |  |
| CC  | -----  |   |     |  |
| EMBL  | X70900; CAA50256.1; -  |   |     |  |
| PIR   | S33777; S33777.  |   |     |  |
| MRSP  | P00763; IDPO.  |   |     |  |
| DR  | InterPro; IPR009003; Cys Ser trypsin.  |   |     |  |
| DR  | InterPro; IPR001254; Peptidase_S1  |   |     |  |
| DR  | InterPro; IPR001314; Peptidase_S1a   |   |     |  |
| DR  | InterPro; IPR001190; Srcr_receptor.  |   |     |  |
| DR  | Pfam; PF00089; trypsin; 1.   |   |     |  |
| DR  | PRINTS; PR00722; CHYMOTRYPSIN.   |   |     |  |
| DR  | SMART; SM00202; SR; 1.   |   |     |  |
| DR  | SMART; SM00020; Tryp_SPC; 1.   |   |     |  |
| DR  | PROSITE; PS00240; TRYPSIN_DOM; 1.  |   |     |  |
| DR  | PROSITE; PS00134; TRYPSIN_HIS; 1.  |   |     |  |
| DR  | PROSITE; PS00135; TRYPSIN_SER; 1.  |   |     |  |
| KW  | Hydrolase; Serine protease; Transmembrane; Signal-anchor.  |   |     |  |
| FT  | CHAIN 1 161  |   |     |  |
| FT  | SERINE PROTEASE HEPsin, NON-CATALYTIC  |   |     |  |
| FT  | CHAIN (POTENTIAL).   |   |     |  |
| FT  | SERINE PROTEASE HEPsin, CATALYTIC CHAIN  |   |     |  |
| FT  | (POTENTIAL).   |   |     |  |
| FT  | CYTOPLASMIC (POTENTIAL).   |   |     |  |
| FT  | SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)   |   |     |  |
| FT  | (POTENTIAL).   |   |     |  |
| FT  | EXTRACELLULAR (POTENTIAL).   |   |     |  |
| FT  | SERINE PROTEASE.   |   |     |  |
| FT  | CHARGE RELAY SYSTEM (BY SIMILARITY).   |   |     |  |
| FT  | CHARGE RELAY SYSTEM (BY SIMILARITY).   |   |     |  |
| FT  | CHARGE RELAY SYSTEM (BY SIMILARITY).   |   |     |  |
| FT  | INTERCHAIN (BY SIMILARITY).  |   |     |  |
| FT  | BY SIMILARITY.   |   |     |  |
| FT  | DISULFID 187 203   |   |     |  |
| FT  | DISULFID 321 337   |   |     |  |
| FT  | DISULFID 348 380   |   |     |  |
| FT  | CARBOHYD 111 111   |   |     |  |
| SQ  | SEQUENCE 416 AA; 44926 MW; E5A9F8FA9550E180 CRC64;   |   |     |  |
| Query Match 26.8%; Score 654.5; DB 1; Length 416;                 |  |   |     |  |
| Best Local Similarity 35.3%; Pred. No. 7.7e-48;                   |  |   |     |  |
| Matches 146; Conservative 61; Mismatches 156; Indels 51; Gaps 10; |  |   |     |  |
| QY  | 60   | ILALATGLGHFDCSGKYCRSFKCIELIARCDGVSDCKGDEYRCVRYGQNAVLOV      | 119 |  |
| Db  | 17   | VAALTVGTLLELTGIG-----AASWAIVTILLR-----SDQELVQLSPGDSRLIVL    | 65  |  |
| QY  | 120  | -PTAASWKTMCSDDWKGHYANVACQLQFPYVSSDNLRVSSLEGQFPREEFVSID----- | 173 |  |
| Db  | 66   | DKTEGTWRLCGRSARNAVAGLCBEMGFLRALAHSELDVETAGANGTSFGFCVDEGLP   | 125 |  |
| QY  | 174  | ---HLLPDDKVTALHSHVYVREGCASGHVVTLOCTACGHRRGYSRIYGVGNLSLSPWP  | 230 |  |
| Db  | 126  | LAQRLL--DVISVC-----DCPRGRFLTATCCQGRKL.PVDRIVGGDSSLGRWEP     | 175 |  |



|   |      |   |                                     |
|---|------|---|-------------------------------------|
| CARBOHYD  | 751  | 751   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| CARBOHYD  | 770  | 770   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| CARBOHYD  | 791  | 791   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| CARBOHYD  | 897  | 897   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| CARBOHYD  | 936  | 936   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| CARBOHYD  | 999  | 999   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| SEQUENCE  | 1069 | AA; 118735 MW; E62549E463743C3D CRC64;                        |                                     |
| Query Match   |      |   |                                     |
| Best Local Similarity 37.4%; Pred. No. 4.6e-47;                   |      |   |                                     |
| Matches 151; Conservative 65; Mismatches 142; Indels 46; Gaps 17; |      |   |                                     |
| Qy  | 67   | LGTHFDC-SGKYCRSFSFKIELIARCDGVSCKGDEYRCVR-----VGGONAVLOVFT     | 121                                 |
| Db  | 682  | LGIPFCQDDEFQCKOG-NCIPLGNLCDSYPHCRDGSDEASCVRFLNGTRSNNGLVQFNI   | 740                                 |
| Qy  | 122  | AASWKTWCSDWKGHYANVACAQLGPFPSYVSDNLRVSSLEGQFREEFVSIIDHLLPDDKV  | 181                                 |
| Db  | 741  | HSIWHIACAENWTQISNEVCHLLGLGS--ANSSMPISTGG---GPFVRVNO-----      | 788                                 |
| Qy  | 182  | TALHHSVYVREG--CASGHVYVTLQCT--ACGHRH---GYSSRIVGGNMSLLSQWPMQASL | 234                                 |
| Db  | 789  | APNGSLILTPSLQCSODSLLILQCNHKSCEKKTKQKVSFKIVGGSDAQAGAWPWVAL     | 847                                 |
| Qy  | 235  | QFQGYH-----LCGGSVITELWIIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-A    | 282                                 |
| Db  | 848  | ---YHRDRSTDRLLCGASLVSDWLVSAHCVYRRNLDPTRTAVLGLHMQSNLTSPQV      | 903                                 |
| Qy  | 283  | PSHLVEKIVYHSKYPKRLGNDIALMKLAGPLTFNEMIQVCLPNSSENEFPDCKVCWTSQ   | 342                                 |
| Db  | 904  | VRRVVDQIVINPHYDRRRKNDIAMHLEFKVNYTDIQCIPLEENQIFIPGRTCSIAG      | 963                                 |
| Qy  | 343  | WGATE-DGGDASPVLNHAAPVLISNKTICNHR-DVYGGIISPSMLCAGYLTGGVDSQCGDS | 400                                 |
| Db  | 964  | WGDKINAGSTVDVLKEADVPLISNEKCCQQLPEYN--ITESMTCAGYBEGGIDSCQGS    | 1021                                |
| Qy  | 401  | GGPLVCQERLWKLVGATSGICGCAEVNKPQVTVRTVTSFLDWIH                  | 444                                 |
| Db  | 1022 | GGPLMCQENNRWFLVGVTSFGVQCALFNHPGVYVRVVSQFIEMIH                 | 1065                                |

Search completed: May 5, 2004, 15:47:20  
Job time : 19 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:40:30 ; Search time 60 Seconds  
(without alignments)  
2133.234 Million cell updates/sec

Title: us-09-846-512-2

Perfect score: 2443

Sequence: 1 MGNDPPAVAPFSRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID      | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1          | 2443  | 100.0       | 453    | 4 AAU29055 | Human PRO   |
| 2          | 2443  | 100.0       | 453    | 4 AAU29055 | Human mem   |
| 3          | 2443  | 100.0       | 453    | 5 ABO18402 | Human ser   |
| 4          | 2443  | 100.0       | 453    | 5 ABJ05565 | Breast ca   |
| 5          | 2443  | 100.0       | 453    | 5 AAU23020 | Human try   |
| 6          | 2443  | 100.0       | 453    | 6 ABU58431 | Human PRO   |
| 7          | 2443  | 100.0       | 453    | 6 ABU87979 | Novel hum   |
| 8          | 2443  | 100.0       | 453    | 6 ABU84294 | Human sec   |
| 9          | 2443  | 100.0       | 453    | 6 ABR66168 | Human sec   |
| 10         | 2443  | 100.0       | 453    | 6 ABR65558 | Human sec   |
| 11         | 2443  | 100.0       | 453    | 6 ABU99498 | Human sec   |
| 12         | 2443  | 100.0       | 453    | 6 ABU82737 | Human PRO   |
| 13         | 2443  | 100.0       | 453    | 6 ABU89858 | Novel hum   |
| 14         | 2443  | 100.0       | 453    | 6 ABR58549 | Human can   |
| 15         | 2443  | 100.0       | 453    | 6 ABR68107 | Human sec   |
| 16         | 2443  | 100.0       | 453    | 6 ABU96160 | Novel hum   |
| 17         | 2443  | 100.0       | 453    | 6 ABU92591 | Human sec   |
| 18         | 2443  | 100.0       | 453    | 6 ABO08668 | Human sec   |
| 19         | 2443  | 100.0       | 453    | 6 ABO02720 | Human sec   |
| 20         | 2443  | 100.0       | 453    | 6 ABR74874 | Human sec   |
| 21         | 2443  | 100.0       | 453    | 6 ABR94636 | Human sec   |
| 22         | 2443  | 100.0       | 453    | 6 ABO25196 | Novel hum   |
| 23         | 2443  | 100.0       | 453    | 6 ABU85609 | Human PRO   |
| 24         | 2443  | 100.0       | 453    | 6 ABU98769 | Novel hum   |
| 25         | 2443  | 100.0       | 453    | 6 ABU97984 | Novel hum   |

|    |      |       |     |            |           |
|----|------|-------|-----|------------|-----------|
| 26 | 2443 | 100.0 | 453 | 6 ABU91690 | Novel hum |
| 27 | 2443 | 100.0 | 453 | 6 ABU72202 | Novel hum |
| 28 | 2443 | 100.0 | 453 | 6 ABU83983 | Human PRO |
| 29 | 2443 | 100.0 | 453 | 6 ABU86224 | Human sec |
| 30 | 2443 | 100.0 | 453 | 6 ABU67437 | Human sec |
| 31 | 2443 | 100.0 | 453 | 6 ABU80465 | Human PRO |
| 32 | 2443 | 100.0 | 453 | 6 ABR99383 | Human sec |
| 33 | 2443 | 100.0 | 453 | 6 ABR98773 | Human sec |
| 34 | 2443 | 100.0 | 453 | 6 ABO16296 | Human sec |
| 35 | 2443 | 100.0 | 453 | 6 ABR92196 | Human sec |
| 36 | 2443 | 100.0 | 453 | 6 ABO18837 | Human sec |
| 37 | 2443 | 100.0 | 453 | 6 ABR78258 | Human sec |
| 38 | 2443 | 100.0 | 453 | 6 ABU56617 | Lung canc |
| 39 | 2443 | 100.0 | 453 | 6 ABU84994 | Novel hum |
| 40 | 2443 | 100.0 | 453 | 6 ABO00133 | Novel hum |
| 41 | 2443 | 100.0 | 453 | 6 ABO11465 | Human sec |
| 42 | 2443 | 100.0 | 453 | 6 ABO02110 | Human sec |
| 43 | 2443 | 100.0 | 453 | 6 ABU88684 | Novel hum |
| 44 | 2443 | 100.0 | 453 | 6 ABU83379 | Human sec |
| 45 | 2443 | 100.0 | 453 | 6 ABO06180 | Novel hum |

## ALIGNMENTS

## RESULT 1

AAU29055

ID AAU29055 standard; protein; 453 AA.

XX AAU29055;

AC AAU29055;

XX 18-DEC-2001 (first entry)

XX Human PRO polypeptide sequence #32.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;

XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;

XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 06-MAR-2000; 2000US-0189688P.

XX 14-MAR-2000; 2000US-0189320P.

XX 15-MAR-2000; 2000US-0189328P.

XX 21-MAR-2000; 2000US-0190828P.

XX 21-MAR-2000; 2000US-0191007P.

XX 21-MAR-2000; 2000US-0191048P.

XX 21-MAR-2000; 2000US-0191314P.

XX 28-MAR-2000; 2000US-0192655P.

XX 29-MAR-2000; 2000US-0193032P.

XX 29-MAR-2000; 2000US-0193053P.

XX 30-MAR-2000; 2000WO-US008439.

XX 04-APR-2000; 2000US-0194449P.

XX 04-APR-2000; 2000US-0194647P.

XX 11-APR-2000; 2000US-0195975P.

XX 11-APR-2000; 2000US-0196000P.

XX 11-APR-2000; 2000US-0196187P.

XX 11-APR-2000; 2000US-0196820P.

XX 18-APR-2000; 2000US-0198121P.

XX 18-APR-2000; 2000US-0198585P.

XX 25-APR-2000; 2000US-0199397P.

PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199554P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 FI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX N-PSDB; AAS45956.  
 DR WPI; 2001-602745/68.  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX Claim 11; Fig 64; 774pp; English.  
 PS Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC animal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX SQ Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 4; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-188;  
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPFAVEAPFRRSLFGLDDLKISFPADADAVAAQILSLPLKFFPIIVIGIALI 60  
 Db 1 MGENDPFAVEAPFRRSLFGLDDLKISFPADADAVAAQILSLPLKFFPIIVIGIALI 60  
 Qy 61 LALAIGLGIHPDCSGKTKRSSFRCIELIARCDGVSDCKGDEYRCVRVGGQNAVLOVF 120  
 Db 61 LALAIGLGIHPDCSGKTKRSSFRCIELIARCDGVSDCKGDEYRCVRVGGQNAVLOVF 120  
 Qy 121 TAASWKTCSDDWKGHYANVACAQLGPFVSYNLRVSSLEGQFREFFVSIDHLLPDDK 180  
 Db 121 TAASWKTCSDDWKGHYANVACAQLGPFVSYNLRVSSLEGQFREFFVSIDHLLPDDK 180  
 Qy 181 VTALHSHVYVREGCASHVVTLOCTACRRRGYSRVVGGNMSLLSQWPQASLQFGYH 240  
 Db 181 VTALHSHVYVREGCASHVVTLOCTACRRRGYSRVVGGNMSLLSQWPQASLQFGYH 240  
 Qy 241 LCGGSVITPLMIITAAHCYVDLYLPKSWTIQVGLVSLLDNPPAPSHLVEKIYTHSKYKPKR 300  
 Db 241 LCGGSVITPLMIITAAHCYVDLYLPKSWTIQVGLVSLLDNPPAPSHLVEKIYTHSKYKPKR 300  
 Qy 301 LGNDIALMKLAGPLTNEIWPVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHAA 360

Db 301 LGNDIALMKLAGPLTNEIWPVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHAA 360  
 Qy 361 VPLISNKCINHRDVGIIISPSMLCAGYLTGGVDSQCGDGGPLVCQERRLKLVGATSF 420  
 Db 361 VPLISNKCINHRDVGIIISPSMLCAGYLTGGVDSQCGDGGPLVCQERRLKLVGATSF 420  
 Qy 421 GIGCAEVNKPQVYTRVTSFLDWIHEQWERDLKT 453  
 Db 421 GIGCAEVNKPQVYTRVTSFLDWIHEQWERDLKT 453

RESULT 2  
 AA06935  
 ID AA06935 standard; protein; 453 AA.  
 XX AA06935;  
 AC AA06935;  
 XX 16-OCT-2001 (first entry)  
 DT Human membrane-type serine protease (MTSP) 6.  
 DE Human; transmembrane serine protease; membrane-type serine protease;  
 KW MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic;  
 KW lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 XX Domain 48..68  
 FT /label= Transmembrane\_domain  
 FT Domain 72..108  
 FT /label= LDLRa\_domain  
 FT /note= "LDL receptor domain class a"  
 FT Domain 109..1205  
 FT /label= SR\_domain  
 FT /note= "Scavenger receptor Cys-rich domain"  
 FT Domain 216..443  
 FT /note= "Trypsin-like serine protease domain"  
 FT Cleavage-site 216..217  
 FT Domain 217..443  
 FT /label= Protease\_domain  
 FT Misc-difference 324  
 FT /note= "Unpaired cysteine"  
 XX WO200157194-A2.  
 PN 09-AUG-2001.  
 XX 02-FEB-2001; 2001WO-US003471.  
 XX 03-FEB-2000; 2000US-0179982P.  
 PR 18-FEB-2000; 2000US-0183542P.  
 PR 22-JUN-2000; 2000US-0231124F.  
 PR 26-JUL-2000; 2000US-0220970F.  
 PR 08-SEP-2000; 2000US-00657986.  
 PR 22-SEP-2000; 2000US-0234840F.  
 XX (CORV-) CORVAS INT INC.  
 PA Madison EL, Ong EO, Yeh J;  
 PI WPI; 2001-488877/53.  
 XX N-PSDB; AAD13118.  
 DR Novel single chain polypeptide comprising protease domain of type-II  
 PT membrane-type serine protease or its catalytically active portion useful  
 PT for treating and preventing cancer and tumor.  
 XX Claim 128; Page 214-215; 256pp; English.  
 PS The invention relates to transmembrane serine proteases and their  
 XX corresponding nucleotides and the protease domain of a type-II membrane-  
 CC

CC type serine protease (MTSP). MTSP is useful for identifying compounds  
 CC that modulate or inhibit its proteolytic activity and for formulating a  
 CC medicament for treating neoplastic disease. MTSP and its corresponding  
 CC nucleotides are useful in preventing or treating tumours or cancers such  
 CC as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in  
 CC diagnostics and in hybridisation assays. MTSP is useful as a diagnostic  
 CC marker for tumour development, growth and/or progression and as  
 CC immunogens to generate antibodies that specifically bind to it. MTSP DNA  
 CC is useful in a yeast two-hybrid system and in gene therapy. The present  
 CC sequence is human MTSP6 protein  
 XX  
 SQ Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 4; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-188;  
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGENDPPAVEAPFSPFSLFGLDLDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIALLI 60  
 DB 1 MGENDPPAVEAPFSPFSLFGLDLDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIALLI 60  
 QY 61 LALAIGLGIHFDCSGKYRCRSSFKEIILARCDGVSDCKDGEDEYRCVVRGGQNAVLOVF 120  
 DB 61 LALAIGLGIHFDCSGKYRCRSSFKEIILARCDGVSDCKDGEDEYRCVVRGGQNAVLOVF 120  
 QY 121 TAASWKTMCDDWKGHYANVACAOQFPSPVSSDNLRVSSLEQGFREEFVSDHLLPDDK 180  
 DB 121 TAASWKTMCDDWKGHYANVACAOQFPSPVSSDNLRVSSLEQGFREEFVSDHLLPDDK 180  
 QY 181 VTALHSHVYVREGCASHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLQFGYH 240  
 DB 181 VTALHSHVYVREGCASHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLQFGYH 240  
 QY 241 LCGSVITPLWIIITAAHCYVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKR 300  
 DB 241 LCGSVITPLWIIITAAHCYVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKR 300  
 QY 301 LGNDIALMKLAGPLTFNEMIOPVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHA 360  
 DB 301 LGNDIALMKLAGPLTFNEMIOPVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHA 360  
 QY 361 VPLISNKNICNHRDVGIIISPSMLCAGYLTGGVDSQQGSGGFLVCQERRLWKLVGATSF 420  
 DB 361 VPLISNKNICNHRDVGIIISPSMLCAGYLTGGVDSQQGSGGFLVCQERRLWKLVGATSF 420  
 QY 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453  
 DB 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453

## RESULT 3

AAO18402  
 ID AAO18402 standard; protein; 453 AA.

AC AAO18402;

DT 11-OCT-2002 (first entry)

DE Human serine protease MP493.

XX Human; serine protease; MP493; cancer; kidney disease; lung disease;  
 KW protein coordinate data; cytostatic; antiasthmatic; antiallergic;  
 KW antiinflammatory; virucide; immunomodulator.

OS Homo sapiens.

PN WO200259295-A1.

PD 01-AUG-2002.

XX 23-JAN-2002; 2002WO-JP000465.

XX 23-JAN-2001; 2001JP-00014963.

XX (MOCH ) MOCHIDA PHARM CO LTD.  
 PA Nakamura Y, Sugano S, Matsusue T, Okamoto A, Okawa K;  
 XX WPI; 2002-566849/60.  
 DR N-PSDB; AAL48490.  
 XX Transmembrane serine protease MP493 for diagnosis of and developing drugs  
 PT for cancer, kidney diseases and lung diseases e.g. asthma, allergy,  
 PT bronchitis, pneumonectasis, pancreatitis and nephritis.  
 XX Claim 3; Page 155-156; 163pp; Japanese.

XX The present invention provides the protein and coding sequences of a  
 CC human serine protease designated MP493. The sequences can be used in the  
 CC diagnosis of and development of drugs for treating cancer, kidney and  
 CC lung diseases, for example asthma, allergy, bronchitis, pneumonectasis,  
 CC viral diseases, shock, multiple organ failure, pancreatitis and  
 CC nephritis. The present sequence is the protein of the invention  
 XX  
 SQ Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 5; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-188;  
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGENDPPAVEAPFSPFSLFGLDLDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIALLI 60  
 DB 1 MGENDPPAVEAPFSPFSLFGLDLDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIALLI 60  
 QY 61 LALAIGLGIHFDCSGKYRCRSSFKEIILARCDGVSDCKDGEDEYRCVVRGGQNAVLOVF 120  
 DB 61 LALAIGLGIHFDCSGKYRCRSSFKEIILARCDGVSDCKDGEDEYRCVVRGGQNAVLOVF 120  
 QY 121 TAASWKTMCDDWKGHYANVACAOQFPSPVSSDNLRVSSLEQGFREEFVSDHLLPDDK 180  
 DB 121 TAASWKTMCDDWKGHYANVACAOQFPSPVSSDNLRVSSLEQGFREEFVSDHLLPDDK 180  
 QY 181 VTALHSHVYVREGCASHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLQFGYH 240  
 DB 181 VTALHSHVYVREGCASHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLQFGYH 240  
 QY 241 LCGSVITPLWIIITAAHCYVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKR 300  
 DB 241 LCGSVITPLWIIITAAHCYVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKR 300  
 QY 301 LGNDIALMKLAGPLTFNEMIOPVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHA 360  
 DB 301 LGNDIALMKLAGPLTFNEMIOPVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHA 360  
 QY 361 VPLISNKNICNHRDVGIIISPSMLCAGYLTGGVDSQQGSGGFLVCQERRLWKLVGATSF 420  
 DB 361 VPLISNKNICNHRDVGIIISPSMLCAGYLTGGVDSQQGSGGFLVCQERRLWKLVGATSF 420  
 QY 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453  
 DB 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453

## RESULT 4

ABU05565

ID ABU05565 standard; protein; 453 AA.

XX ABU05565;

XX 14-NOV-2002 (first entry)

DE Breast cancer-associated protein 30.

XX Breast cancer; breast cancer-associated gene sequence; drug development;  
 KW pharmacogenetics; biosensor development.

OS Unidentified.  
XX FN W0200259377-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002242.  
XX PR 24-JAN-2001; 2001US-0263965P.  
XX PR 02-FEB-2001; 2001US-0265928P.  
XX PR 09-APR-2001; 2001US-00829472.  
XX PR 09-APR-2001; 2001US-0282698P.  
XX PR 04-MAY-2001; 2001US-0288590P.  
XX PR 29-MAY-2001; 2001US-0294443P.  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX PI Mack DH, Gish KC, Afar D;  
XX DR WPI; 2002-583738/62.  
XX DR N-PSDB; ABO7722.  
XX XX  
XX PT Detecting a breast cancer-associated transcript in a patient's cell,  
XX FT useful for diagnosing breast cancer, comprises contacting a biological  
XX PT sample with a polynucleotide that selectively hybridizes with breast  
XX PT cancer nucleic acids.  
XX XX  
XX PS Disclosure; Page 373; 414pp; English.  
XX XX  
XX CC The invention comprises a method of detecting a breast cancer-associated  
XX CC transcript in a cell from a patient. The method of the invention involves  
XX CC contacting a biological sample from the patient with a nucleotide that  
XX CC hybridizes to one of the 69 breast cancer-associated gene sequences shown  
XX CC in the specification. The method of the invention is useful in the  
XX CC diagnosis or prognosis of breast cancer, and for detecting genes that are  
XX CC up or down-regulated in breast cancer cells. Genes identified by the  
XX CC method of the invention can be used in diagnostic purposes and also as  
XX CC targets for screening for therapeutic compounds that modulate breast  
XX CC cancer (e.g. hormones or antibodies). Identification of genes that are  
XX CC over or under expressed in breast cancer can additionally provide high-  
XX CC resolution, high-sensitivity datasets which can be used in the areas of  
XX CC diagnostics, therapeutics, drug development, pharmacogenetics, protein  
XX CC structure and biosensor development. Amino acid sequences AB05536 -  
XX CC AB05604 represent the proteins encoded by the 69 breast cancer-  
XX CC associated genes of the invention  
XX XX  
SQ Sequence 453 AA;  
Query Match 100.0%; Score 2443; DB 5; Length 453;  
Best Local Similarity 100.0%; Pred No. 3.8e-188;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGNDPPAVAPSPFRSLFGLDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIILI 60  
Db 1 MGNDPPAVAPSPFRSLFGLDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIILI 60  
Qy 61 LALAIGLGIHFDGSGKRCSSFKCIELIARCDSVDCDGEDEYRCVAVGGNAVLOVF 120  
Db 61 LALAIGLGIHFDGSGKRCSSFKCIELIARCDSVDCDGEDEYRCVAVGGNAVLOVF 120  
Qy 121 TAASWTKMCSDDMKGHYANVACAQLGPPSYVSSDNLRVSSLEQCFREEFVSDHLLPDDK 180  
Db 121 TAASWTKMCSDDMKGHYANVACAQLGPPSYVSSDNLRVSSLEQCFREEFVSDHLLPDDK 180  
Qy 181 VTALHHSVYVREGCASHVVTLOCTACGHRGYSRRIVGGNMSLLSQWPQASLQPGYH 240  
Db 181 VTALHHSVYVREGCASHVVTLOCTACGHRGYSRRIVGGNMSLLSQWPQASLQPGYH 240  
Qy 241 LCGSVITPLWIITAAHCYVDLYLPSKSWTIQVGLVSLDNPAPSHLVKIVYHSKYKPKR 300  
Db 241 LCGSVITPLWIITAAHCYVDLYLPSKSWTIQVGLVSLDNPAPSHLVKIVYHSKYKPKR 300  
Qy 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSSENFDPGKVCWTSWGATEDGGDASPVNLHAA 360

Db 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSSENFDPGKVCWTSWGATEDGGDASPVNLHAA 360  
Qy 361 VPLISNKICNHRDVGIIISPSMLCAGYLTGGVDSQGGSGGGLVCQERRLWKLVGATSF 420  
Db 361 VPLISNKICNHRDVGIIISPSMLCAGYLTGGVDSQGGSGGGLVCQERRLWKLVGATSF 420  
Qy 421 GIGCAEVNKGQVTRVTSFLDWIHEQWERDLKT 453  
Db 421 GIGCAEVNKGQVTRVTSFLDWIHEQWERDLKT 453  
RESULT 5  
AAE23020  
ID AAE23020 standard; protein; 453 AA.  
XX AC AAE23020;  
XX DT 21-AUG-2002 (first entry)  
XX DE Human trypsin family member, 14094 protein #1.  
XX KW Human; 14094 protein; trypsin family; proliferation; tumour; carcinoma;  
XX KW metastatic lesion; cancer; lung; breast; ovarian; liver; colon; sarcoma;  
XX KW signal transduction; apoptosis; necrosis; cytosolic; enzyme.  
XX OS Homo sapiens.  
XX FH  
XX Key Location/Qualifiers  
FT Region 1..47  
FT Modified-site /note= "Non-transmembrane region"  
FT Domain 14..16  
FT Domain /note= "Protein kinase C phosphorylation site"  
FT Region 48..69  
FT Region /note= "Transmembrane domain"  
FT Domain 70..453  
FT Domain /note= "Non-transmembrane region"  
FT Modified-site /note= "Low-density lipoprotein (LDL) receptor domain class A"  
FT Modified-site 74..76  
FT Modified-site /note= "Protein kinase C phosphorylation site"  
FT Modified-site 82..84  
FT Modified-site /note= "Protein kinase C phosphorylation site"  
FT Modified-site 94..99  
FT Modified-site /note= "N-myristylation site"  
FT Modified-site 99..105  
FT Domain /note= "Tyrosine kinase phosphorylation site"  
FT Modified-site 110..205  
FT Modified-site /note= "Scavenger receptor cysteine-rich domain"  
FT Modified-site 111..116  
FT Modified-site /note= "N-myristylation site"  
FT Modified-site 124..126  
FT Modified-site /note= "Protein kinase C phosphorylation site"  
FT Modified-site 159..162  
FT Modified-site /note= "Casein kinase II phosphorylation site"  
FT Modified-site 193..198  
FT Modified-site /note= "N-myristylation site"  
FT Modified-site 214..216  
FT Domain /note= "Protein kinase C phosphorylation site"  
FT Region 216..443  
FT Region /note= "Trypsin domain"  
FT Modified-site 216..220  
FT Modified-site /note= "Proteolytic activator site"  
FT Modified-site 219..224  
FT Modified-site /note= "N-myristylation site"  
FT Modified-site 221..224  
FT Disulfide-bond /note= "N-glycosylation site"  
FT Region 242..258  
FT Modified-site 253..258  
FT Modified-site /note= "Matches PS00134"  
FT Modified-site 276..279  
FT Modified-site /note= "Casein kinase II phosphorylation site"

FT Modified-site 302..307 /note= "N-myristylation site"  
 FT Modified-site 315..318 /note= "Casein kinase II phosphorylation site"  
 FT Disulfide-bond 338..406  
 FT Modified-site 341..344 /note= "Glycosaminoglycan attachment site"  
 FT Modified-site 365..367 /note= "Protein kinase C phosphorylation site"  
 FT Disulfide-bond 369..385 /note= "N-myristylation site"  
 FT Modified-site 391..396 /note= "N-myristylation site"  
 FT Disulfide-bond 396..424 /note= "Matches PS00135"  
 FT Region 398..402 /note= "N-myristylation site"  
 FT Modified-site 421..426 /note= "N-myristylation site"  
 FT Modified-site 438..441 /note= "Casein kinase II phosphorylation site"  
 FT W0200183781-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 30-APR-2001; 2001WO-US013903.  
 XX  
 XX 28-APR-2000; 2000US-0200621P.  
 XX 08-AUG-2000; 2000US-00633300.  
 XX (MTEL-) MILLENNIUM PHARM INC.  
 XX  
 XX Meyers R, Macbeth KJ;  
 PI  
 XX WPI; 2002-147444/19.  
 DR N-PSDB; AAD36726.  
 XX  
 XX Novel polypeptide, 14094, which is a human trypsin family member useful  
 PT for treating and preventing a disorder such as cancer of the lung,  
 PT breast, ovary, liver and colon.  
 XX  
 XX Claim 8; Page 113; 140pp; English.  
 PS  
 XX The invention relates to an isolated polypeptide, designated 14094, which  
 CC is a human trypsin family member. The invention is especially useful in  
 CC screening assays such as those to identify compounds that modulate their  
 CC activity or expression. The compound is used to inhibit proliferation, or  
 CC induce the killing, of a 14094-expressing hyperproliferative cell (such  
 CC as that found in a solid tumour, a soft tissue tumour, or a metastatic  
 CC lesion, preferably a cancer selected from a sarcoma, a carcinoma, and an  
 CC adenocarcinoma where the cancer is selected from lung cancer, breast  
 CC cancer, ovarian cancer, liver cancer and colon cancer). The compound may  
 CC be used to treat or prevent a disorder characterised by aberrant cellular  
 CC proliferation or differentiation of a 14094-expressing cell such as that  
 CC above, where the subject is a mammal, preferably a human. The compound  
 CC may be selected from a peptide, a polypeptide, a small organic  
 CC molecule, a small inorganic molecule and an antibody to modulate 14094 or  
 CC an antisense, a ribozyme, or a triple helix molecule for modulation of  
 CC 14094 DNA. Preferably, (for modulation of the protein) the compound is an  
 CC antibody conjugated to a therapeutic moiety selected from a cytotoxin, a  
 CC cytotoxic agent and a radioactive metal ion. In addition, the compound  
 CC may be administered in combination with a cytotoxic agent. The cytotoxic  
 CC agent may be selected from an antimicrotubule agent, a topoisomerase I  
 CC inhibitor, a topoisomerase II inhibitor, a mitotic inhibitor, an  
 CC antimetabolite, an alkylating agent, an intercalating agent, an agent  
 CC capable of interfering with signal transduction pathway, an agent that  
 CC promotes apoptosis or necrosis and radiation. The present sequence is  
 CC human 14094 protein  
 XX  
 XX Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 5; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 3,8e-188;  
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |               |   |     |
|----|-----|---------------|---|-----|
| QY | 1   | MGENDPPAVEAPF | SRSLFGLDDLKISPVAPDADAAQAQILSLPLKFFPIIVIGIALL        | 60  |
| DB | 1   | MGENDPPAVEAPF | SRSLFGLDDLKISPVAPDADAAQAQILSLPLKFFPIIVIGIALL        | 60  |
| QY | 61  | LALAIGLIIHFD  | CSGKYRCRSSFKEIILIAICDGVSDCKDGEDEYRCVVRGGQNAVLOVF    | 120 |
| DB | 61  | LALAIGLIIHFD  | CSGKYRCRSSFKEIILIAICDGVSDCKDGEDEYRCVVRGGQNAVLOVF    | 120 |
| QY | 121 | TAAASKWTCSD   | DKWGHYANVACAQLGFPSSVSSDNLRVSSLEGOFREFFVSIIDHLLPDDK  | 180 |
| DB | 121 | TAAASKWTCSD   | DKWGHYANVACAQLGFPSSVSSDNLRVSSLEGOFREFFVSIIDHLLPDDK  | 180 |
| QY | 181 | VTALHHSVYV    | REGCASGHVVTLOCTACGHRGYSRRIVGGMNLSLLSQWPAQASLQFGQYH  | 240 |
| DB | 181 | VTALHHSVYV    | REGCASGHVVTLOCTACGHRGYSRRIVGGMNLSLLSQWPAQASLQFGQYH  | 240 |
| QY | 241 | LCGGSVITPL    | MIITAAHCVDYDLYLPKSWTIQVGLVSLLDNPAFSLHVEKLVYHSKYKPKR | 300 |
| DB | 241 | LCGGSVITPL    | MIITAAHCVDYDLYLPKSWTIQVGLVSLLDNPAFSLHVEKLVYHSKYKPKR | 300 |
| QY | 301 | LGNDIALM      | KLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGMGATEDGGDASVNLHAA | 360 |
| DB | 301 | LGNDIALM      | KLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGMGATEDGGDASVNLHAA | 360 |
| QY | 361 | VPLISN        | KICNHRDYGIIISPSMLCAGYLTGGVDSCOGSGPLVCOERRLKLVGATSF  | 420 |
| DB | 361 | VPLISN        | KICNHRDYGIIISPSMLCAGYLTGGVDSCOGSGPLVCOERRLKLVGATSF  | 420 |
| QY | 421 | GIGCAEVN      | KPGVYTRVTSFSLDWIHEQMERDLKT                          | 453 |
| DB | 421 | GIGCAEVN      | KPGVYTRVTSFSLDWIHEQMERDLKT                          | 453 |

RESULT 6  
 ABUS9431  
 ID ABUS8431 standard; protein; 453 AA.  
 XX  
 AC ABUS8431;  
 XX  
 DT 15-APR-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #32.  
 XX  
 KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
 KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003027272-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 21-JUN-2002; 2002US-00176492.  
 XX  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 28-OCT-1997; 97US-0063540P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 29-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068817P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 20-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081049P.  
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PR 09-APR-1998; 98US-0081195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083559P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088032P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088555P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 11-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089090P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0090246P.  
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PR 22-JUN-1998; 98US-0090254P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090461P.  
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PR 25-JUN-1998; 98US-0090676P.  
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PR 25-JUN-1998; 98US-0090690P.  
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PR 25-JUN-1998; 98US-0090695P.  
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PR 26-JUN-1998; 98US-00105413.  
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PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0091010P.  
PR 01-JUL-1998; 98US-0091359P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.  
PR 02-JUL-1998; 98US-0091626P.  
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PR 24-JUL-1998; 98US-0094006P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 10-AUG-1998; 98US-0095998P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
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PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 01-SEP-1998; 98US-0098716P.  
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PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
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PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100649P.  
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PR 18-SEP-1998; 98US-0101068P.  
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PR 23-SEP-1998; 98US-0101472P.  
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|  |              |  |
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| PR   | 05-JUN-1998; | 98US-0088167P.   |
| PR   | 05-JUN-1998; | 98US-0088202P.   |
| PR   | 05-JUN-1998; | 98US-0088212P.   |
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| PR   | 05-JUN-1998; | 98US-0088552P.   |
| PR   | 09-JUN-1998; | 98US-0088722P.   |
| PR   | 10-JUN-1998; | 98US-0088738P.   |
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| PR   | 10-JUN-1998; | 98US-0088825P.   |
| PR   | 10-JUN-1998; | 98US-0088826P.   |
| PR   | 11-JUN-1998; | 98US-0088861P.   |
| PR   | 11-JUN-1998; | 98US-0088863P.   |
| PR   | 11-JUN-1998; | 98US-0088876P.   |
| PR   | 12-JUN-1998; | 98US-0089090P.   |
| PR   | 12-JUN-1998; | 98US-0089105P.   |
| PR   | 16-JUN-1998; | 98US-0089512P.   |
| PR   | 16-JUN-1998; | 98US-0089514P.   |
| PR   | 17-JUN-1998; | 98US-0089538P.   |
| PR   | 17-JUN-1998; | 98US-0089598P.   |
| PR   | 17-JUN-1998; | 98US-0089653P.   |
| PR   | 18-JUN-1998; | 98US-0089908P.   |
| PR   | 18-JUN-1998; | 98US-0089952P.   |
| PR   | 19-JUN-1998; | 98US-0090246P.   |
| PR   | 22-JUN-1998; | 98US-0090252P.   |
| PR   | 22-JUN-1998; | 98US-0090354P.   |
| PR   | 22-JUN-1998; | 98US-0090429P.   |
| PR   | 24-JUN-1998; | 98US-0090435P.   |
| PR   | 24-JUN-1998; | 98US-0090444P.   |
| PR   | 24-JUN-1998; | 98US-0090461P.   |
| PR   | 24-JUN-1998; | 98US-0090535P.   |
| PR   | 24-JUN-1998; | 98US-0090540P.   |
| PR   | 25-JUN-1998; | 98US-0090576P.   |
| PR   | 25-JUN-1998; | 98US-0090678P.   |
| PR   | 25-JUN-1998; | 98US-0090688P.   |
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| PR   | 25-JUN-1998; | 98US-0090696P.   |
| PR   | 26-JUN-1998; | 98US-0090822P.   |
| PR   | 26-JUN-1998; | 98US-0090863P.   |
| PR   | 26-JUN-1998; | 98US-0091010P.   |
| PR   | 01-JUL-1998; | 98US-0091359P.   |
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| DB   | 1            | MGENDPRAVEAFPSRSLFGDLDLKISPVAPDADAVAQAQILSLPLKFFPIIVIGIITALI 60  |
| QY   | 61           | LALAIGLIHFDGSGKYRCRSSFKEIILIARCDCGVSDCKGDEYRCVVRVGGQNAVLOVF 120  |
| DB   | 61           | LALAIGLIHFDGSGKYRCRSSFKEIILIARCDCGVSDCKGDEYRCVVRVGGQNAVLOVF 120  |
| QY   | 121          | TAASWKTCSDDWKHYANVACQIAGFSPSYSSDNLVSSILEGOFREEFYSIDHLLPDDK 180   |
| DB   | 121          | TAASWKTCSDDWKHYANVACQIAGFSPSYSSDNLVSSILEGOFREEFYSIDHLLPDDK 180   |
| QY   | 181          | VTALHSHVYVREGCASGHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLOFGYH 240     |
| DB   | 181          | VTALHSHVYVREGCASGHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLOFGYH 240     |
| QY   | 241          | LCGGSVITPLMIITAAHCVDYLYLPKSWTIQVGLVSLDDNPAPSHLYEKIYVHSHKYPKR 300 |
| DB   | 241          | LCGGSVITPLMIITAAHCVDYLYLPKSWTIQVGLVSLDDNPAPSHLYEKIYVHSHKYPKR 300 |
| QY   | 301          | LGNDIALMKLAGPLTFNEMIQVCLPNSEENFPDGKVCWTSGWGTEDGGDASPVLNHAA 360   |
| DB   | 301          | LGNDIALMKLAGPLTFNEMIQVCLPNSEENFPDGKVCWTSGWGTEDGGDASPVLNHAA 360   |
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| DB   | 361          | VPLISNKICNHRDVGIIISPSMLCAGYLTGCVDSQDSCGGPLVCQBRRLKVLGATSF 420    |
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XX DT 02-AUG-2003 (first entry)  
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XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing.  
XX OS Homo sapiens.  
XX PN US2003032112-A1.  
XX PD 13-FEB-2003.  
XX PF 21-JUN-2002; 2002US-00176756.  
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Qy 61 LALAIGLGIHDCSGKRCRSSFKEILIAKCDGVSCCKGDEBYRCVRVGGQNAVLOVF 120
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RESULT 9
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XX AC ABR66168;
XX DT 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO382, SEQ ID NO:64.
XX KW Human; PRO; secreted protein; transmembrane protein;
XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX KW adrenal tumour; lung; colon; breast; kidney; rectum; cervix;
XX KW liver; drug screening; transgenic animal; genetic analysis;
XX KW antiarthritic; vulnerary; gene therapy.
XX OS Homo sapiens.
XX PN US2003027278-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176987.
XX PR 18-SEP-1997; 97US-0059263P.
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DB 301 LGNDIALMKLAGLTFNEMIQPVCLPNSEENPPDGKVCWTSGWGATEGGDASPVLNHAA 360
QY 361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGVVSDCQDGGGGLVCGQERRLKLVGATSF 420
DB 361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGVVSDCQDGGGGLVCGQERRLKLVGATSF 420
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DT 09-AUG-2003 (first entry)
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Query Match 100.0%; Score 2443; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.ee-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGENDPPAVAPPSFRSLFGLDLDLKISPVAPDADAVAAQILSLPLKFPPIIVIGIILI 60
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XX KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX KW chromosome mapping; gene mapping; cytostatic.
XX OS Homo sapiens.
XX PN US2003032113-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176911.
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Best Local Similarity 100.0%; Pred. No. 3.8e-188;

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RESULT 13
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XX AC ABU89858;
XX DT 11-AUG-2003 (first entry)
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XX KW Novel human secreted and transmembrane protein PRO382.
XX KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.
XX OS Homo sapiens.
XX PN US2003036147-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187741.
XX PR 18-SEP-1997; 97US-0059263P.
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XX PF
XX 17-SEP-2002; 2002WO-US029560.
XX 17-SEP-2001; 2001US-0323469P.
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XX 12-APR-2002; 2002US-0372246P.
XX PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnick A;
XX DR WPI; 2003-354600/33.
XX DR N-PSDB; ACC72670.
XX PT
XX PT New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX PS Claim 12; Page 736-737; 767pp; English.
XX CC The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR58521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,
XX CC atherosclerosis and endometriosis. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX SQ Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.8e-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TAASWKTMCSDDKWGHYANVACQLOFPSPVSSDNLRVSSLEQCFREEFVSDHLLPDDK 180
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RESULT 15
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XX AC ABR68107;
XX DT 11-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO382, SEQ ID NO:64.
XX KW Human; PRO; secreted protein; transmembrane protein;
XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX KW liver; drug screening; transgenic animal; genetic analysis;
XX KW antiarthritic; vulnery; gene therapy.
XX OS Homo sapiens.
XX PN US2003027264-A1.
XX PD 06-FEB-2003.
XX 18-JUN-2002; 2002US-00174579.
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PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101739P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101922P.  
PR 25-SEP-1998; 98US-0101786P.  
PR 25-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 2443; DB 6; Length 453;  
Best Local Similarity 100.0%; Pred. No. 3.8e-188;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed May 5 15:56:14 2004

us-09-846-512-2.rag

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | MGENDPPEAPPSFRSLFGLDLDLKISPVAPDADAVAAQILSLPLKFPPIIVIGIALL     | 60  |
| Db | 1   | MGENDPPEAPPSFRSLFGLDLDLKISPVAPDADAVAAQILSLPLKFPPIIVIGIALL     | 60  |
| Qy | 61  | LALAIGLGHFDCSGKRCRSSFKEIELIARCDSKDEGEDEYRCVGVGQNAVLOVF        | 120 |
| Db | 61  | LALAIGLGHFDCSGKRCRSSFKEIELIARCDSKDEGEDEYRCVGVGQNAVLOVF        | 120 |
| Qy | 121 | TAASWKTMCSDDMKGYHANYACALGPPSYVSSDNLRVSSLEQFPREEFVSIIDHLLPDDK  | 180 |
| Db | 121 | TAASWKTMCSDDMKGYHANYACALGPPSYVSSDNLRVSSLEQFPREEFVSIIDHLLPDDK  | 180 |
| Qy | 181 | VTALHHSVYVREGGASGHVVTLOCTACGHRGYSRRIVGGMNLSLLSQWPMQASLQFQGYH  | 240 |
| Db | 181 | VTALHHSVYVREGGASGHVVTLOCTACGHRGYSRRIVGGMNLSLLSQWPMQASLQFQGYH  | 240 |
| Qy | 241 | LCGGSVITPLWIIITAAHCVVDLYLPKSWTIQVGLVSLLDNPPAPSHLVEKIVYHSHKPKR | 300 |
| Db | 241 | LCGGSVITPLWIIITAAHCVVDLYLPKSWTIQVGLVSLLDNPPAPSHLVEKIVYHSHKPKR | 300 |
| Qy | 301 | LGNDIALMKLAGPLTFNEMIQFVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHAA  | 360 |
| Db | 301 | LGNDIALMKLAGPLTFNEMIQFVCLPNSSENFDPGKVCWTSGWGATEDGGDASPVLNHAA  | 360 |
| Qy | 361 | VPLISNKNHRDYGIIISPSMLCAGYLTGGVDSQQDSGGPLVCOERLWKLVGATSF       | 420 |
| Db | 361 | VPLISNKNHRDYGIIISPSMLCAGYLTGGVDSQQDSGGPLVCOERLWKLVGATSF       | 420 |
| Qy | 421 | GIGCAEVNKGYYTRVTSFLDWIHEQMERDLKT                              | 453 |
| Db | 421 | GIGCAEVNKGYYTRVTSFLDWIHEQMERDLKT                              | 453 |

Search completed: May 5, 2004, 15:46:51  
Job time : 63 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:44:20 ; Search time 45 Seconds  
(without alignments)  
3176.217 Million cell updates/sec

Title: US-09-846-512-2  
Perfect score: 2443  
Sequence: 1 MGENDPPEVAPFSLFLG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:  
1: sp archaea:  
2: sp bacteria:  
3: sp fungi:  
4: sp human:  
5: sp invertebrate:  
6: sp mammal:  
7: sp mhc:  
8: sp organelle:  
9: sp phase:  
10: sp plant:  
11: sp rodent:  
12: sp virus:  
13: sp vertebrate:  
14: sp unclassified:  
15: sp xvirus:  
16: sp bacteriap:  
17: sp archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 2225  | 91.1        | 453    | 11 Q812A6 | Q812A6 mus musculus |
| 2          | 1682  | 68.8        | 344    | 4 Q8WY52  | Q8WY52 homo sapien  |
| 3          | 882   | 36.1        | 492    | 4 Q96T73  | Q96T73 homo sapien  |
| 4          | 877   | 35.9        | 490    | 11 Q7TN04 | Q7TN04 mus musculus |
| 5          | 875.5 | 35.8        | 490    | 11 Q920K3 | Q920K3 rattus norv  |
| 6          | 836   | 34.2        | 767    | 13 Q9DGR2 | Q9DGR2 xenopus lae  |
| 7          | 813   | 33.3        | 326    | 13 Q7Z280 | Q7Z280 brachydanio  |
| 8          | 726.5 | 29.7        | 581    | 4 Q8YBE2  | Q8YBE2 homo sapien  |
| 9          | 720.5 | 29.5        | 471    | 11 Q8CFR0 | Q8CFR0 mus musculus |
| 10         | 718.5 | 29.4        | 558    | 4 Q86YM4  | Q86YM4 homo sapien  |
| 11         | 711   | 29.1        | 537    | 4 Q9BEV1  | Q9BEV1 homo sapien  |
| 12         | 704.5 | 28.8        | 445    | 11 Q8CJ17 | Q8CJ17 rattus norv  |
| 13         | 700.5 | 28.7        | 371    | 11 Q8CJ16 | Q8CJ16 rattus norv  |
| 14         | 693.5 | 28.4        | 455    | 11 Q8CDR0 | Q8CDR0 mus musculus |
| 15         | 657.5 | 26.9        | 777    | 11 Q8CAN9 | Q8CAN9 mus musculus |
| 16         | 656.5 | 26.9        | 405    | 4 Q96E86  | Q96E86 homo sapien  |

Q97506 sus scrofa  
Q8ROP5 mus musculus  
Q8B1X6 mus musculus  
Q8ET26 homo sapien  
Q8VJ74 rattus norv  
Q8B210 mus musculus  
Q9AJ55 anopheles g  
Q9NAT0 anopheles g  
Q9JJ17 rattus norv  
Q8B204 mus musculus  
Q9YIV3 polyandroca  
Q9DGR1 xenopus lae  
Q8VDV1 mus musculus  
Q8VHK8 mus musculus  
Q8VVC1 homo sapien  
Q9QZ74 rattus norv  
Q8QV88 mus musculus  
Q9VSU0 drosophila  
Q9UL12 drosophila  
Q8IQB8 drosophila  
Q9UL13 drosophila  
Q9B119 drosophila  
Q960G6 drosophila  
Q9VSU2 drosophila  
Q9XZM7 strongyloce  
Q8QYN4 rattus norv  
Q8BHM9 mus musculus  
Q8OZ40 rattus norv  
Q8AVB0 brachydanio

ALIGNMENTS

RESULT 1  
Q812A6 PRELIMINARY; PRT; 453 AA.  
ID Q812A6;  
AC Q812A6;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Transmembrane proteinase tmprss3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rao N.V., Rao G.N., Hoidal J.R.;  
RT "Genomic Organization of Murine Transmembrane Proteinases.";  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF479687; AAO33581.1;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0005044; F:scavenger receptor activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys Ser\_trypsin.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase SLA.  
DR InterPro; IPR001190; Srcr\_receptor.  
DR Pfam; PF00057; ldl\_recept\_a; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00192; LDLa; 1.  
DR SMART; SM00202; SR; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS01209; LDLRA\_1; 1.  
DR PROSITE; PS50068; LDLRA\_2; 1.  
DR PROSITE; PS50287; SRCR\_2; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.



DR PROSITE; PS00135; TRYPSIN SER; 1.  
SQ SEQUENCE 453 AA; 49505 MW; 1E7ECD6CB3DD894 CRC64;

Query Match 91.1%; Score 2225; DB 11; Length 453;  
Best Local Similarity 89.0%; Pred. No. 6.3e-207;  
Matches 403; Conservative 25; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGENDPFAVEAPFSPRLFGDLDDKISPVAPADAVAAQILSLPLKFFPIIVIGIIALI 60  
DB 1 MGENDPFAVEAPFSPRLFGDLDDKISPVAPDGAVAQAQILSLPLKFFPIIVIGIIALI 60

QY 61 LALAIGLGHFDGSGKYRCRSPFKCIETIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVF 120  
DB 61 LALAIGLGHFDGSGKYRCRSPFKCIETIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVF 120

QY 121 TAASWTKMCDMDKGVANVACQAQLGFPSPVSSDNLRVSSLEGGQFEEFVSIIDHLLPDDK 180  
DB 121 TAASWTKMCDMDKGVANVACQAQLGFPSPVSSDHLRVDALEEQGDGFVSIINHLSDDK 180

QY 181 VTALHSHVYVREGCAGSHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLOFQGYH 240  
DB 181 VTALHSHVYVREGCAGSHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLOFQGYH 240

QY 241 LCGSVITPLMIITAAHCYVDLVPKSWTIQVGLVSLDNPAPSHLVEKIVVHSYKPKR 300  
DB 241 LCGSVITPLMIITAAHCYVDLVPKSWTIQVGLVSLDNPAPSHLVEKIVVHSYKPKR 300

QY 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSBENFPDGKVCWTSGMGATEDGDDASPVLNHAA 360  
DB 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSBENFPDGKVCWTSGMGATEDGDDASPVLNHAA 360

QY 361 VPLISNKICNHRDVGIIISPSMLCAGYLTVGGVSDCGSGGGLVCOERLAKLVGATSF 420  
DB 361 VPLISNKICNHRDVGIIISPSMLCAGYLTVGGVSDCGSGGGLVCOERLAKLVGATSF 420

QY 421 GIGCAEVNKEGVYTRVTSFLDVIHEQMERDLKT 453  
DB 421 GIGCAEVNKEGVYTRVTSFLDVIHEQMERDLKT 453

RESULT 2  
Q8WY52  
ID Q8WY52 PRELIMINARY; PRT; 344 AA.  
AC Q8WY52;  
DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Potential serine protease TMRPS3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yang Y.C., Chen S.Y., Chang M.S.;  
RT "Cloning and characterization of TMRPS3, a new member of the serine  
protease family."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL: AF267741; AAL56664.1; -;  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0004263; F:chymotrypsin activity; IEA.  
DR GO: GO:0008233; F:peptidase activity; IEA.  
DR GO: GO:0005044; F:scavenger receptor activity; IEA.  
DR GO: GO:0004295; F:trypsin activity; IEA.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR009003; Cys Ser trypsin.  
DR InterPro: IPR002172; LBL\_receptor\_A.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR InterPro: IPR001190; Scrv receptor.  
DR Pfam: PF00057; ldl\_recept\_a; 1.  
DR Pfam: PF00089; trypsin; 1.

PRINTS; PRO0722; CHYMOTRYPSIN.  
DR SMART; SM00192; LDLa; 1.  
DR SMART; SM00202; SR; 1.  
DR SMART; SM00202; Tryp\_SPC; 1.  
DR PROSITE; PS01209; LDLa\_1; 1.  
DR PROSITE; PS00068; LDLa\_2; 1.  
DR PROSITE; PS00287; SRCR\_2; 1.  
DR PROSITE; PS02040; TRYPSIN DOM; 1.  
DR PROSITE; PS00134; TRYPSIN HIS; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 344 AA; 37447 MW; 0A88BF289972F8BF CRC64;

Query Match 58.8%; Score 1682; DB 4; Length 344;  
Best Local Similarity 95.2%; Pred. No. 2e-154; 9; Indels 4; Gaps 1;  
Matches 319; Conservative 3; Mismatches 3;

QY 1 MGENDPFAVEAPFSPRLFGDLDDKISPVAPADAVAAQILSLPLKFFPIIVIGIIALI 60  
DB 1 MGENDPFAVEAPFSPRLFGDLDDKISPVAPDGAVAQAQILSLPLKFFPIIVIGIIALI 60

QY 61 LALAIGLGHFDGSGKYRCRSPFKCIETIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVF 120  
DB 61 LALAIGLGHFDGSGKYRCRSPFKCIETIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVF 120

QY 121 TAASWTKMCDMDKGVANVACQAQLGFPSPVSSDNLRVSSLEGGQFEEFVSIIDHLLPDDK 180  
DB 121 TAASWTKMCDMDKGVANVACQAQLGFPSPVSPDLRVSSLEGGQFEEFVSIIDHLLPDDK 180

QY 181 VTALHSHVYVREGCAGSHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLOFQGYH 240  
DB 181 VTALHSHVYVREGCAGSHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLOFQGYH 240

QY 241 LCGSVITPLMIITAAHCYVDLVPKSWTIQVGLVSLDNPAPSHLVEKIVVHSYKPKR 300  
DB 241 LCGSVITPLMIITAAHCYVDLVPKSWTIQVGLVSLDNPAPSHLVEKIVVHSYKPKR 300

QY 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSBENFPDGKVCWTSGMGATEDGDDASPVLNHAA 360  
DB 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSBENFPDGKVCWTSGMGATEDGDDASPVLNHAA 360

RESULT 3  
Q96T73  
ID Q96T73 PRELIMINARY; PRT; 492 AA.  
AC Q96T73;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Epitheliasin.  
GN TMRPS2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=21223025; PubMed=11322890;  
RX Jacquinet E., Rao N.V., Rao G.V., Wang Z., Albertine K.H.,  
RA Hoidal J.R.;  
RT "Cloning and characterization of the cDNA and gene for human  
epitheliasin."  
RL Eur. J. Biochem. 268:2687-2699(2001).  
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL: AF329454; AAK53559.1; -;  
DR HSP; P00761; IAN1.  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0004263; F:chymotrypsin activity; IEA.  
DR GO: GO:0008233; F:peptidase activity; IEA.  
DR GO: GO:0005044; F:scavenger receptor activity; IEA.  
DR GO: GO:0004295; F:trypsin activity; IEA.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR009003; Cys\_Ser trypsin.  
DR InterPro: IPR002172; LBL\_receptor\_A.



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=83355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20363741; PubMed=10903452;  
RA Yamada K., Takabatake T., Takeshima K.;  
RT "Isolation and characterization of three novel serine protease genes  
from *Xenopus laevis*.";  
RL Gene 252:209-216(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AB038497; BAB08217.1; --  
DR HSSP; P00766; 1CHG.  
DR MEROPS; S01.049; --  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00057; ldl\_recept\_a; 4.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00089; trypsin; 1.  
DR PRINTS; PR00261; LDLRECEPTOR.  
DR SMART; SM00192; LDLA; 8.  
DR SMART; SM00020; tryp\_Spc; 1.  
DR PROSITE; PS01209; LDLRA\_1; 8.  
DR PROSITE; PS50068; LDLRA\_2; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 767 AA; 86001 MW; E0566A38796DE95E CRC64;

Query Match 34.2%; Score 836; DB 13; Length 767;  
Best Local Similarity 45.1%; Pred. No. 7.1e-72;  
Matches 175; Conservative 46; Mismatches 131; Indels 36; Gaps 9;

QY 78 RCSSPKCIELIARCDGVSDCKGDEYRCVYRGQNAVLOVF--TAASWKTCSDDDWK 135  
DB 394 RCGSSVSCVLSQWCDGVSDCPYGEDEMSCVSLYPADFLQVISTVSAMLPVCSDTWND 453  
QY 136 HYANVACAQLGF--PSYVSSDNLK-----VSSLEGQFEEFVSIDHLLPDDKVTALH 185  
DB 454 DGRFACQDFGNGSSYNYRDTLMSYPAPNGYFKLYSGYWSKF-----YTSVQ 502  
QY 186 HSYYREGCASHVTVLQCTACG-HRRGYSSRIYVGNMSSLQWQASLQFGYHLGG 244  
DB 503 YSSY----CYSGNVVSLHICSGVSNNSLVSRIVGGTFANLGNWPNQVNLQYITGVJCGG 558  
QY 245 SVITPLWITIAAHCVVDLYLPKS-WTIQVLVSLDNP---APSHLVEKIVVHSKYKPK 299  
DB 559 SIISPKWIVTAACHVYGVSSASGRVFG--TLTKPSYNNASAYFERIIVHPGKSY 615  
QY 300 RLGNIDIALMKLAGPLTFNEMIQVCLPNSSENFDPDGKVCWTSGHGATEDGGDASFLNHA 359  
DB 616 TVDNDIALMKLRDEITFGYTTQVCLPNSGMFWEAGTTTWSHGSTYEGGSVSTYLOYA 675  
QY 360 AVPLISNKICNHRDYYGGIISPSMLCAGVLTGGVDSCOGSDGGLVCCQERLWLKLVGATS 419  
DB 676 APLIDSNVCNOSYVINGQITSSMICAGVLTGGVDTCQDGGGLVKNKNTWLVGDT 735

Query Match 35.8%; Score 875.5; DB 11; Length 490;  
Best Local Similarity 44.7%; Pred. No. 5.7e-76;  
Matches 182; Conservative 62; Mismatches 144; Indels 19; Gaps 10;

QY 52 IVIGTIALIALGLGIHF---DC-SGKYRCSPKCIELIARCDGVSDCKGDEYRC 107  
DB 88 LALGLSPVAAGAALLKFWDSKCSSEMECGSGTCTSSSLGDCGVAQCPNGKDNRC 147  
QY 108 VRYGGQNAVLOVFTA--ASKWTKCSDWKGHYANVACAQLGFP-SYVSSDNLRYSSLEGQ 164  
DB 148 VRIYGSFTLQVYSSORKAWPYCQDDWNEVGRACKDMGYNKFSYSGIPDSGATS 207  
QY 165 FREEFVSIDHLLPDDKVTALHSHVYVREGCASHVTVLQCTACGHR-GYSSRIYVGNMS 223  
DB 208 FMKLNVSAGNV---DLYKKLYHS-----DSCSRMVVSLRACIECGVRSVRQSRIVGGSTA 260  
QY 224 LLSQWPNQASLQFGVHLGGSVITPLWITIAHCYVD-LYLPKSWITQVGLV--SLLDN 280  
DB 261 SPGDWPNQVSLHVGQHLVCGGSIITFEWIVTAHCVSEPLSPRYTAFAGLKKSLMFY 320  
QY 281 PAPSHLVEKIVYHSKYKPKELGNIDIALMKLAGPLTFNEMIQVCLPNSSENFDPDGKVCWT 340  
DB 321 -GSRHQVEKIVISHPNYDSKTKNNDIALMKLQTLPLAFNDVVPKVLNPGMMLDLAQECWI 379  
QY 341 SGHGATEDGGDASFLNHAAPVLSNKICNHRDYYGGIISPSMLCAGVLTGGVDSCOGSD 400  
DB 380 SGMGATYEXKTSVDLNAAMPVLEPSKNSKIYNNLTIPAMITPAMICAGFIQGSVDSCOGSD 439  
QY 401 GGPLVCCERLWLKLVGATSGFSGICAEVKNKPGVYTRVTSFLDWIHEQM 447  
DB 440 GGPLVTLKNEIWLIGDTSWGSCAKAYRPGVYGVNTVFTDMLYQGM 486

RESULT 6  
Q9DGR2 ID Q9DGR2 PRELIMINARY; PRT; 767 AA.  
AC Q9DGR2;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Embryonic serine protease-2.  
GN XESP-2.  
OS Xenopus laevis (African clawed frog).

AC Q7Z80;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE SI:dz69G10.3 (Novel protein similar to human transmembrane protease,  
DE serine 3 (TMPRSS3)) (Fragment).  
GN SI:dz69G10.3.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Corby N.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL672083; CAB61105.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0005044; F:scavenger receptor activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Scrv\_receptor.  
DR InterPro; IPR001190; Scrv\_receptor.  
DR Pfam; PF00057; ldl\_recept\_a; 1.  
DR Pfam; PF00089; trypsin\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00192; LDLA; 1.  
DR SMART; SM00202; SR; 1.  
DR SMART; SM00202; Tryp\_Spc; 1.  
DR PROSITE; PS01209; LDLRA\_1; 1.  
DR PROSITE; PS00068; LDLRA\_2; 1.  
DR PROSITE; PS50287; SRCR\_2; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Transmembrane; Protease.  
FT NON TER 1  
SQ SEQUENCE 326 AA; 35561 MW; 8D6F12214393CDB2 CRC64;  
  
Query Match 33.3%; Score 813; DB 13; Length 326;  
Best Local Similarity 42.6%; Pred. No. 3.8e-70;  
Matches 160; Conservative 47; Mismatches 101; Indels 68; Gaps 4;  
  
QY 73 CSKYRCRSPKCIELIARCDGVSDCKDGEYRCVRVGQNAVLFQVFTAAASWKTMSDD 132  
DB 5 CSKFKHCVSVRCISRNACDGVQDCRDGEDELNCVRVSGSHSVLVQFGRGLMRTVCSG 64  
  
QY 133 WKGHYANVACQLGFPSPSTVSSDNLRSVLSLEQGFREEFVSDHLLPDDKVTAHSHSVYRE 192  
DB 65 WDSQLSTLACRLQGY----- 79  
  
QY 193 GCASHVVTLOCTACGHRGYSRIRVGNMSSLQWPQWASLOFGYHLCGGSVITPLWI 252  
DB 80 -----SRSAISRIVGNVSKSQVPMQVSLHYQNYLCCGSIISSEWI 123  
  
QY 253 ITAAHCYVDLYLPKSWTTIQGLVSLNDNPASHLVEKIVYHSKYKPKRLGNDIALMKLAG 312  
DB 124 LTAACHVFGFAQVPLWDVYAGLINPLLSKAEAHSEKIIYHANFRSKSFSDYIALIKLT 183  
  
QY 313 PLTENMTQVCLPNSSENFDPGKVCWTSWGATEDGGDASPVLNHAAPLISNKICNHR 372  
DB 184 PLTFNDQIAPICLPNIGSFNGQCLISGNGATVDSGETSLSHVQVPLLSNKEKRL 243  
  
QY 373 DVIYGIISFSLCAGYLTGGVDSQGGSPVLCQERRLWLKVGATFGIGCAEVNKPVG 432  
DB 244 G-----LNNWNVCTEFLR-GVGTQCGDGGPLAQCGSAWTLVGTGWDNCNGKVNKPGI 296  
  
QY 433 YTRVTSFLDWDHEQNE 448

DB 297 YTSISEALTWIEQWE 312  
  
RESULT 8  
Q9BYE2  
ID Q9BYE2 PRELIMINARY; PRT; 581 AA.  
AC Q9BYE2;  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Membrane-type mosaic serine protease.  
GN MSPL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Lung;  
RX MEDLINE=21167393; PubMed=11267681;  
RA Kim D.R., Sharmin S., Incue M., Kido H.;  
RT "Cloning and expression of novel mosaic serine proteases with and  
RT without a transmembrane domain from human lung.";  
RL Biochim. Biophys. Acta 1518:204-209 (2001).  
DR EMBL; AB048796; BAB39741.1; -.  
DR HSP; P00763; IDPO.  
DR MEROPS; S01.087; -.  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR001190; Scrv\_receptor.  
DR Pfam; PF00057; ldl\_recept\_a; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00192; LDLA; 1.  
DR SMART; SM00202; SR; 1.  
DR SMART; SM00202; Tryp\_Spc; 1.  
DR PROSITE; PS50287; SRCR\_2; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 581 AA; 62689 MW; 4DABE24D7D5B4A4 CRC64;  
  
Query Match 29.7%; Score 726.5; DB 4; Length 581;  
Best Local Similarity 38.2%; Pred. No. 2e-61;  
Matches 158; Conservative 66; Mismatches 161; Indels 29; Gaps 10;  
  
QY 44 LPLKFPPIVIGIILALALALGIGHDC-----SGKYRCRSPKCIELIARCDGVSDCK 99  
DB 161 LPL-----IGCVLLIALVLSLILFQWQGTGIRHKQRESCPKHAVRCDDGVDDCK 213  
  
QY 100 DGEDEYRCVRVGQNAVLFQVFTAAAS--WKTMSDDWKGHYANVACQLGFPSPYSSDNL 157  
DB 214 LKSDGLGCVRPDWDKSLKIYSGSSHQWLPICSSNNDSYSEKTCRQLGFSAHRTTEVA 273  
  
QY 158 VSSLEQGFREEFVSDHLLPDDKVTAHSHSVYRCGASHVVTLOCTACGHRGYSRI 217  
DB 274 -----HRDFANFSILRYN--STIQESLR-RSHCPQSQRVVISLQCSHCG-LRAMTGR 321  
  
QY 218 VGNMSSLQWPQWASLOFGYHLCGGSVITPLWITAAHCYVDL--YLPKSWTTIQGLV 275  
DB 322 VGGALASDSKMPQVSLHFGTHICGGLIDAQWLTAAHCFVTRKVLGKMKVYAGTS 381  
  
QY 276 SLIDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGLTFNEMIQVCLPNSSENFDPG 335  
DB 382 NLHQLPEASIAE--IINSNYTDEDDVDIALMRLSKPLTLSAHIPACLPVHGQTFSLN 440  
  
QY 336 KVCWTSWGATEDGGD-ASPVLNHAAPLISNKICNHRDVGVIISPSMLCAGYLTGGVD 394

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Db 441 ETCWITGKTRTDKTSFPLREVQVNLIDFKCNDYLYDYLTPRMWACGLHGGSD 500
Qy 395 SCQDSSGGLVCCERRLKLVGATSGIGCAEVNKGQVYTRVTSPLDWIHEQWE 448
Db 501 SCQDSSGGLVCCQNNRWYLAGVTSWGTGCGQNKGVYTKVTEVPLNYSKME 554

RESULT 9
Q8CFEO PRELIMINARY; PRT; 471 AA.
ID Q8CFEO AC Q8CFEO
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Similar to mosaic serine protease (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042878; AA042878.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00530; SRCR; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0287; SRCR_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
FT NON_TER
SQ SEQUENCE 471 AA; 52535 MW; ED58CFE6B7C3BCC4 CRC64;

Query Match 29.5%; Score 720.5; DB 11; Length 471;
Best Local Similarity 35.6%; Pred. No. 5.9e-61;
Matches 163; Conservative 74; Mismatches 176; Indels 45; Gaps 11;

Qy 24 LKISPV-----APDADVAQAQLSLPLKFFP-----IVIGIILALIAIG 66
Db 26 VRATPVGAIPRASPAPSPATRESPLGSPFKFSWQETQRQLPLIGCVILLISLVIS 85
Qy 67 LGIHFDGCKYRCSSFK-----CTELIARCDGSDCKDGEYRCVRVGGONAVLOV 119
Db 86 LILLFYP---WEGHTGIKYEPLESCPIHVRCDGVVDCKWDELCCVRFWDKSLKV 142
Qy 120 PTAAS--WKTMCSDDWKGYHANVACAQLGPPSVSSDNLRVSSLEGQFREEFVSDHLLP 177
Db 143 YSGSGGWLPCVSSSWNDTSKRTCCQLGFDPSAYRTTEVAHRDITTSF-----LL 192
Qy 178 DDKVTALHVSYYVEGASGHVVTLOCTACGHRGVSSRIIVGGNMSSLQMPWQASIQEQ 237
Db 193 SEYNTTQESLY-RSQCFSPRYVSLQSHCG-LRAMTGRIVGGALTSKWPQVSLHFG 250
Qy 238 GYHLGCGSVITPLMIITAAHCYVDL--YLPKSWTIQVGLVSLDNPAPSLVKIVYHSK 295

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Db 251 TTHTCGGTLDAQVWLTAAHCFFVTRKLEGGKVVAGTGNLHQLPEAS-ISOIINGN 309
Qy 296 YPKRLGNLIALMKIAGPLTFNEMIQVCLPNSSEENPPDGKVCWTSCWGATEDGGD-ASP 354
Db 310 YTDQDDYDIALIRLSKPLTSAHIHPACLPMEHQFFGLNETCWTGFGTKETDEKTS 369
Qy 355 VINHAAPVPLISNKICNHRDVGIIISPSMLCAGYLTGGVDSQQDSSGGLVCCERRLKL 414
Db 370 FLREVQVNLIDFKCNDYLYDYLTPRMWACGLHGGSDSCQDSSGGLVCCQNNRWY 429
Qy 415 VGATSPGIGCAEVNKGQVYTRVTSPLDWIHEQWERDLK 452
Db 430 AGVTSWGTGCGQNKGVYTKVTEVPLNYSKMESEVR 467

RESULT 10
Q86YM4 PRELIMINARY; PRT; 558 AA.
ID Q86YM4 AC Q86YM4
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Transmembrane protease serine 6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Park T.J.; Park W.J.;
RT "Homo sapiens transmembrane protease, serine 6 (TMPRSS6) mRNA.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY190317; AAC38082.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0287; SRCR_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
SQ SEQUENCE 558 AA; 60432 MW; 4AC817FCD70D7017 CRC64;

Query Match 29.4%; Score 718.5; DB 4; Length 558;
Best Local Similarity 38.5%; Pred. No. 1.2e-60;
Matches 160; Conservative 64; Mismatches 159; Indels 33; Gaps 11;

Qy 44 LPLKFFPIVIGIILALIAIGLGHDFDCSGKY-----RCRSGFKIELIARCDGVSD 97
Db 161 LPL-----IGCVLLIALVLSLILLPQWQGTGIRYKEQRES--CPEHAVRRDGV 211
Qy 98 CKDGEDEYRCVRVGGONAVLOVFTAAS--WKTMCSDDWKGYHANVACAQLGPPSVSSDN 155
Db 212 CKLKSDELGCVRFDWKSLKLIYSGSSHQWLPICSSNNWDSYSEKTCQQLGFESAHTTE 271
Qy 156 LRVSSLEQGFREEFVSDIHLLPDDKVTALHVSYYVEGASGHVVTLOCTACGHRGVSS 215
Db 272 VA-----HRDFANSPSILRYN--STIQESLH-RSECPQRYISLQCHCG-LRAMTG 319
Qy 216 RIVGNNMSSLQMPWQASIQEQVHLGCGSVITPLMIITAAHCYVDL--YLPKSWTIQV 273

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Db      320 RIVGALASDKPWPQVSLHFGTHICGGTLIDAQWLVTAHCFVTRKVLGKMKVYAG 379
QY      274 LVSLNDNPAPSHLVKIVVHSKYPKRLGNDIALMKLAGLPTFNEMIQPVCLPNSSENF 333
Db      380 TSNLHQLPEASIAE--LIINSNTDEDDYDIALMELSKPLTSAHIAHACLPMHGQTF 438
QY      334 DGKVCWTSGWATDGGD--ASPVLNHAAVPLISNKICNHRDVGIIISPSMLCAGVLTGG 392
Db      439 LNETCWITGFKTRETDDKTSPFLREVQVNLIDFKKCNLYVDSYLTFRMWCAGDLRG 498
QY      393 VDSQGGSGGLVCEQERRLWKLVGATSGFGCAEVNKPVGVTTRVTSFLDWIHEOME 448
Db      499 RDSQGGSGGLVCEQERRLWKLVGATSGFGCAEVNKPVGVTTRVTSFLDWIHEOME 554

RESULT 11
Q9BYEI ID Q9BYEI PRELIMINARY; PRT; 537 AA.
AC Q9BYEI
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mosaic serine protease.
GN MSFS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TTSUE=lung;
RX MEDLINE=21167393; PubMed=11267601;
RA Kim D.R., Sharmin S., Inoue M., Kido H.;
RT "cloning and expression of novel mosaic serine proteases with and
RT without a transmembrane domain from human lung.";
RL Biochim. Biophys. Acta 1518:204-209 (2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR ENBL; AB048797; BAB39742.1; -
DR HSSP; P00763; IDPO.
DR MEROPS; S01.087; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0006508; F:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srrc_receptor.
DR Pfam; PF000857; ldl_recept_a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS50287; SRR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 537 AA; 58102 MW; A39FP4E8816DAECF CRC64;

Query Match 29.1%; Score 711; DB 4; Length 537;
Best Local Similarity 39.1%; Pred. No. 5.9e-60;
Matches 146; Conservative 64; Mismatches 145; Indels 18; Gaps 8;

QY 85 CIELIARCDGVSCKDGEYRCVVRGGQNAVLOVFTAA--WKTMCSDDWKGHYANVAC 142
Db 174 CPKHAVRCDGWVDCKLKSDDELGCVRPDWDSLLKIYSGSHQWLPICCSNWNDSYEKTC 233
QY 143 AOLGFPYVSDNLRLVSSLGQPREFVSDHLLPDDKVTALHSHSVYREGCASHGVVIL 202
Db 234 RQLGFESAHTTEVA-----HRDFANGFSILRYN--STIQESLH-RSHCFPSQYISL 282
QY 203 QCTACGHRRGYSSRIYVGNMSSLQWNPQASLOFQGYHLGGSVITPLWITTAHCVYDL 262

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Db      283 QCSFCG-LRAMTGRIVGALASDKPWPQVSLHFGTHICGGTLIDAQWLVTAHCFV 341
QY      263 --YLPKSWTTOVGLVSLDNPAPSHLVKIVVHSKYPKRLGNDIALMKLAGLPTFNEMI 320
Db      342 REKVLGKVKVAGTNSLHQLPEASIAE--LIINSNTDEDDYDIALMELSKPLTSAH 400
QY      321 QPVCLPNSSENFDPKVCWTSGWATDGGD--ASPVLNHAAVPLISNKICNHRDVGII 379
Db      401 HPACLPMHGQTFSLNETCWITGFKTRETDDKTSPFLREVQVNLIDFKKCNLYVDSYL 460
QY      380 SPSMLCAGVLTGGVDSQGGSGGLVCEQERRLWKLVGATSGFGCAEVNKPVGVTTRVTSF 439
Db      461 TPRMWCAGDLHGGSDSCQGGSGGLVCEQERRLWKLVGATSGFGCAEVNKPVGVTTRVTSF 520
QY      440 LDWIHEQMERDLK 452
Db      521 LPWTYKMESEVR 533

RESULT 12
Q8CU17 ID Q8CU17 PRELIMINARY; PRT; 445 AA.
AC Q8CU17
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Adrenal mitochondrial protease long variant.
GN AMP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEBH;
RA Omer S., Bicknell A.B., Lowry P.J.;
RT "Identification of a rat adrenal mitochondrial protease.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF537098; AAN06757.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004283; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS50287; SRR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
SQ SEQUENCE 445 AA; 48440 MW; BE3F56D8372ED988 CRC64;

Query Match 28.8%; Score 704.5; DB 11; Length 445;
Best Local Similarity 35.7%; Pred. No. 1.9e-59;
Matches 148; Conservative 69; Mismatches 169; Indels 29; Gaps 11;

QY 52 IVIGHIALILALATG---LGHFPCSGKYRCRSFKCIELIARCDGVSCKDGEYR-- 106
Db 40 VTILGALGLAGVSGSWLLVLYLWPAASPVPVSVTLQEEVTLSCPGVS---SEKLLPS 95
QY 107 -----CVRVGQNAVLOVFTAA--SWKTCSDDWKGHYANVACQAGPSPVSSDNLRLVS 159
Db 96 LPKAVSFINGEDLLELVQVRAPDNLVLCHEGNPALGMICQSLGLFRITQHKAVNLS 155
QY 160 SLEQGFREFFVSIDHLLPDDKVTALHSHSVYREGCASHGVVITLOCTACGHRRGYSSRI 219

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Db 156 DIKLRSQFAQLS-ARPSLV- --EAWQPTNCPGSRIVSLKSCG-ARPLASRIVG 210
QY 220 GNMSSLQWPQASLOFQGYHLCGGSVITPLIITAAHCVYDLYLPK--SWTIQVGLVSL 277
Db 211 GOAVASGRWQASVNLGSRHTCGGSLVAPYVWVTAACHMYSFRLSRLSSRWVHAGLV- 269
QY 278 LONPASH--LVEKIVHSKYKPKLGNLNDIALMKLAGLPTNEMIQVCLPNSSEFPD 334
Db 270 -HSAVRCHOGTWVEKIPIPHLYSAQNHDYDVALQLRTINFSDTVSAVCLPAKEQHPFQ 328
QY 335 GKVCWTSGWGTEDG- GDASPVNLHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGV 393
Db 329 GSGQVSWGWTGDPSTHSSDTLQDTWVPLSTDLNCSMYSGALTHMLCAGYLDGDA 388
QY 394 DSCQDGGGLVQCBRLMKLVGATSGIGCAEVNKPQGVYTRVTSFLDWIHEQME 448
Db 389 DACQDGGGLVQCBRLMKLVGATSGIGCAEVNKPQGVYTRVTSFLDWIHTVQ 443

RESULT 13
Q8CJ16 PRELIMINARY; PRT; 371 AA.
AC Q8CJ16;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Adrenal mitochondrial protease short variant.
GN AMP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RC SEQUENCE FROM N.A.
RA Omer S., Bicknell A.B., Lowy P.J.;
RT "Identification of a rat adrenal mitochondrial protease.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF537099; AAN06758.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004263; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001190; Srcr receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0287; SRCR 2; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
KW Protease.
SQ SEQUENCE 371 AA; 40694 MW; 89A64081D9A1PE26 CRC64;

Query Match 28.7%; Score 700.5; DB 11; Length 371;
Best Local Similarity 39.7%; Pred. No. 3.7e-59;
Matches 138; Conservative 55; Mismatches 140; Indels 15; Gaps 8;

QY 109 RVGGQNAVLOVFTAA--SWKTCSDDWKGYHANVACAQIGFYSVSSDNLRSVLEGQFR 166
Db 29 RINGEDLLLEVQVRAPDMLLVCHEGWNPALGNHICQSLGYRLTQHKAVNLSDTIKLRN 88
QY 167 EEFVSDIHLPPDDKVTALHSHVYVREGCASGHVVTIQCACGRRGYSRIYVGNMSSL 226
Db 89 QFAQLS-ARPSLV- --EAWQPTNCPGSRIVSLKSCG-ARPLASRIVGQAVASG 143
QY 227 QWPQASLOFQGYHLCGGSVITPLIITAAHCVYDLYLPK--SWTIQVGLVSLDNPAPS 284

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Db 144 RWPQASVLMGSRHTCGGSLVAPYVWVTAACHMYSFRLSRLSSRWVHAGLV- --HSAVRQ 201
QY 285 H---LVEKIVHSKYKPKLGNLNDIALMKLAGLPTNEMIQVCLPNSSEFPDGVKCVWTS 341
Db 202 HQGTWVEKIPIPHLYSAQNHDYDVALQLRTINFSDTVSAVCLPAKEQHPFQSGQCVTS 261
QY 342 GWGATEDG- GDASPVNLHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSQGD 400
Db 262 GWGHTDPSHTHSSDTLQDTWVPLSTDLNCSMYSGALTHMLCAGYLDGADACQGD 321
QY 401 GGLVQCBRLMKLVGATSGIGCAEVNKPQGVYTRVTSFLDWIHEQME 448
Db 322 GGLVQCBRLMKLVGATSGIGCAEVNKPQGVYTRVTSFLDWIHTVQ 369

RESULT 14
Q8CDRO PRELIMINARY; PRT; 455 AA.
AC Q8CDRO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane protease.
GN TMPRSS5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK029714; BAC26577.1; -.
DR MGD; MGI:1933407; Tmprss5.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001190; Srcr receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0287; SRCR 2; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
SQ SEQUENCE 455 AA; 49669 MW; BE22EB2E7503C74B CRC64;

Query Match 28.4%; Score 693.5; DB 11; Length 455;
Best Local Similarity 36.1%; Pred. No. 2.3e-58;
Matches 150; Conservative 63; Mismatches 173; Indels 29; Gaps 11;

QY 52 IVIGITALILALAIG--LGIHPDCSGKRCSSFKIELIARCDGVSDCKDGEYR-- 106
Db 50 VILGVLLAGAGIASMLLVLYLWPPASPSISGTLQEEEMTLNCPGV- --REBELLS 105
QY 107 -----CVRGQNAVLOVFTAA--SWKTCSDDWKGYHANVACAQIGFYSVSSDNLRS 159
Db 106 LPTVTSFRINGEDLLLEVQVRAPDMLLVCHEGWNPALGNHICQSLGYRLTQHKAVNLS 165
QY 160 SLEQPREFEVSDIHLPPDDKVTALHSHVYVREGCASGHVVTIQCACGRRGYSRIYV 219
Db 166 DIKLRSQFAQLS-ARPSLV- --EAWQPTNCPGSRIVSLKSCG-ARPLASRIVG 220

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:45:40 ; Search time 22 seconds  
(without alignments)  
1063.026 Million cell updates/sec

Title: US-09-846-512-2  
Perfect score: 2443  
Sequence: 1 MGENDPPAVEAPFRRSLFG.....TRVTSPLDWIHEQMERDLKT 453

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score  | Length | DB ID | Description        |
|------------|-------------|--------|--------|-------|--------------------|
| 1          | 97.6        | 2385.5 | 454    | 3     | US-09-518-046-2    |
| 2          | 2206        | 90.3   | 455    | 3     | US-09-261-416-2    |
| 3          | 1354        | 55.4   | 294    | 3     | US-09-518-046-4    |
| 4          | 885         | 36.2   | 492    | 3     | US-09-342-749-2    |
| 5          | 885         | 36.2   | 492    | 4     | US-09-691-840-2    |
| 6          | 874         | 35.8   | 492    | 4     | US-09-685-166A-895 |
| 7          | 862         | 35.3   | 157    | 3     | US-09-518-046-23   |
| 8          | 696         | 28.5   | 283    | 4     | US-08-807-151-1    |
| 9          | 696         | 28.5   | 283    | 4     | US-09-478-957-1    |
| 10         | 674         | 27.6   | 417    | 1     | US-08-200-900A-2   |
| 11         | 669.5       | 27.4   | 798    | 5     | PCT-US94-00616-2   |
| 12         | 669.5       | 27.4   | 798    | 5     | US-09-656-002-2    |
| 13         | 665.5       | 27.2   | 423    | 4     | US-09-656-002-2    |
| 14         | 665         | 27.2   | 416    | 2     | US-09-000-846-2    |
| 15         | 658         | 26.9   | 435    | 3     | US-09-008-271A-6   |
| 16         | 658         | 26.9   | 437    | 4     | US-09-851-588-8    |
| 17         | 656.5       | 26.9   | 376    | 4     | US-09-820-002-2    |
| 18         | 656.5       | 26.9   | 406    | 4     | US-09-851-588-6    |
| 19         | 585.5       | 24.0   | 256    | 2     | US-09-027-337-3    |
| 20         | 585.5       | 24.0   | 256    | 4     | US-09-644-600-3    |
| 21         | 585.5       | 24.0   | 256    | 4     | US-09-654-600A-3   |
| 22         | 580.5       | 23.8   | 255    | 3     | US-08-944-483-67   |
| 23         | 579.5       | 23.7   | 638    | 2     | US-08-681-151-3    |
| 24         | 571         | 23.4   | 418    | 1     | US-08-508-448C-25  |
| 25         | 571         | 23.4   | 418    | 4     | US-09-370-838-82   |
| 26         | 571         | 23.4   | 418    | 4     | US-09-370-838-83   |
| 27         | 569         | 23.3   | 418    | 4     | US-09-370-838-62   |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 4, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 895, App  |
|            |             |        |        |       | Sequence 23, Appl  |
|            |             |        |        |       | Sequence 1, Appli  |
|            |             |        |        |       | Sequence 4, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 2, Appli  |
|            |             |        |        |       | Sequence 6, Appli  |
|            |             |        |        |       | Sequence 3, Appli  |
|            |             |        |        |       | Sequence 3, Appli  |
|            |             |        |        |       | Sequence 67, Appl  |
|            |             |        |        |       | Sequence 3, Appli  |
|            |             |        |        |       | Sequence 25, Appl  |
|            |             |        |        |       | Sequence 82, Appl  |
|            |             |        |        |       | Sequence 83, Appl  |
|            |             |        |        |       | Sequence 62, Appl  |

RESULT 1

US-09-518-046-2

/ Sequence 2, Application US/09518046  
/ Patent No. 6294683  
/ GENERAL INFORMATION:  
/ APPLICANT: O'Brien, Timothy J.  
/ APPLICANT: Underwood, Lowell J.  
/ TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed  
/ TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof  
/ FILE REFERENCE: D6192CIP  
/ CURRENT APPLICATION NUMBER: US/09/518,046  
/ CURRENT FILING DATE: 2000-03-02  
/ EARLIER APPLICATION NUMBER: 09/261,416  
/ EARLIER FILING DATE: 1999-03-03  
/ NUMBER OF SEQ ID NOS: 153  
/ SEQ ID NO: 2  
/ LENGTH: 454  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: complete amino acid sequence of TAGD-12  
/ OTHER INFORMATION: protein  
US-09-518-046-2

Query Match 97.6%; Score 2385.5; DB 3; Length 454;  
Best Local Similarity 97.8%; Pred. No. 1.3e-223;  
Matches 444; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

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|----|-----|---------------------|-----------------|-----------------------|---------|-----|
| Qy | 1   | MGENDPPAVEAPFRRSLFG | LDLKI           | SPVAPADAVAAQILSLPLKFF | PTIVIGI | 59  |
| Db | 1   | MGENDPPAVEAPFRRSLFG | LDLKI           | SPVAPADAVAAQILSLPLKFF | PTIVIGI | 60  |
| Qy | 60  | ILALAI              | GLGIFDCSGKRCRSF | FCIELI                | ARC     | 119 |
| Db | 61  | ILALAI              | GLGIFDCSGKRCRSF | FCIELI                | ITR     | 120 |
| Qy | 120 | FTAA                | SKWTWCSD        | DKGHYANVACAQ          | LGPSYSS | 179 |
| Db | 121 | FTAA                | SKWTWCSD        | DKGHYANVACAQ          | LGPSYSS | 180 |
| Qy | 180 | KVTAL               | HSHVYVREGCAS    | GHVVT                 | LQCTAC  | 239 |
| Db | 181 | KVTAL               | HSHVYVREGCAS    | GHVVT                 | LQCTAC  | 240 |
| Qy | 240 | HL                  | CGSVITPLMTIT    | AAHC                  | VDLYL   | 299 |
| Db | 241 | HL                  | CGSVITPLMTIT    | AAHC                  | VDLYL   | 300 |
| Qy | 300 | RL                  | CNDIAL          | MKLAGPL               | TNEMIQ  | 359 |
| Db | 300 | RL                  | CNDIAL          | MKLAGPL               | TNEMIQ  | 359 |

Db 301 RLGNDAIMKLAGPLTFNEMIQPVCLPNESENFPGKVCWTSGWGTEDGGDASPVLNHA 360  
Qy 360 AVPLISNKICNHRDVGIIISPSMLCAGYLTOGVDSQCGDSGGLPVLCQERRLWKLVGATS 419  
Db 361 AVPLISNKICNHRDVGIIISPSMLCAGYLTOGVDSQCGDSGGLPVLCQERRLWKLVGATS 420  
Qy 420 FGIGCAEVNKPVGYYTTRVTSFLDWIHEQMERDLKT 453  
Db 421 FGIGCAEVNKPVGYYTTRVTSFLDWIHEQMERDLKT 454

RESULT 2  
US-09-261-416-2  
; Sequence 2, Application US/09261416A  
; Patent No. 6291663  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Underwood, Lowell J.  
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease  
; TITLE OF INVENTION: Over-expressed in Ovarian Carcinoma  
; FILE REFERENCE: D6192  
; CURRENT APPLICATION NUMBER: US/09/261,416A  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 14  
; SEQ ID NO 2  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of TADG-12 encoded by nucleotides  
; OTHER INFORMATION: 144 to 1511 of Sequence 1  
; Patent No. 6291663  
US-09-261-416-2

Query Match 90.3%; Score 2206; DB 3; Length 455;  
Best Local Similarity 91.7%; Pred. No. 3.7e-206;  
Matches 421; Conservative 5; Mismatches 23; Indels 10; Gaps 3;

Qy 1 MGNDPPAVEAPPSFRSLFGLDLKISPVAPDADAVAAQILSLPLKFF-PIIVIGIIAL 59  
Db 1 MGNDPPAVEAPPSFRSLFGLDLKISPVAPDADAVAAQILSLPLPEVFSQSSSLGIIAL 60  
Qy 60 ILALAIGLGHFDCSGKRCRSSFCKIELTARCDGVSDCKDGEYRCVVRGQNAVLOV 119  
Db 61 ILALAIGLGHFDCSGKRCRSSFCKIELTARCDGVSDCKDGEYRCVVRGQNAVLOV 120  
Qy 120 FTAASWKTMCSDWKGHYANVACAQLGFPSVSSDNLRVSSLEGQFREEFVSDHLLPDD 179  
Db 121 FTAASWKTMCSDWKGHYANVACAQLGFPSVSSDNLRVSSLEGQFREEFVSDHLLPDD 180  
Qy 180 KVTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNLSLLSQWPQASLOFGY 239  
Db 181 KVTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNLSLLSQWPQASLOFGY 240  
Qy 240 HLCGGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLDNDNPAPSHLVKIVHSHYKPK 299  
Db 241 HLCGGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLDNDNPAPSHLVKIVHSHYKPK 300  
Qy 300 RLGNDAIMKLAGPLTFNEMIQPVCLPNESENFPGKVCWTSGWGTEDGGDASPVLNHA 359  
Db 301 RLGNDAIMKLAGPLTFNEMIQPVCLPNESENFPGKVCWTSGWGTEDGGDASPVLNHA 360  
Qy 360 AVPLISNKICNHRDVGIIISPSMLCAGYLTOGVDSQCGDSGGLPVLCQERRLWKL 414  
Db 361 AVPLISNKICNHRDVGIIISPSMLCAGYLTOGVDSQCGDSGGLPVLCQERRLWKL 415  
Qy 415 VGATSFIGCAEVNKPVGYYTTRVTSFLDWIHEQMERDLKT 453  
Db 417 VGATSFIGCAEVNKPVGYYTTRVTSFLDWIHEQMERDLKT 455

RESULT 3

US-09-518-046-4

; Sequence 4, Application US/09518046  
; Patent No. 6294663  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Underwood, Lowell J.  
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed  
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof  
; FILE REFERENCE: D6192CIP  
; CURRENT APPLICATION NUMBER: US/09/518,046  
; CURRENT FILING DATE: 2000-03-02  
; EARLIER APPLICATION NUMBER: 09/261,416  
; EARLIER FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 4  
; LENGTH: 294  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: complete amino acid sequence of TADG-12  
; OTHER INFORMATION: variant protein  
US-09-518-046-4

Query Match 55.4%; Score 1354; DB 3; Length 294;  
Best Local Similarity 88.1%; Pred. No. 1.6e-123;  
Matches 258; Conservative 7; Mismatches 20; Indels 8; Gaps 2;

Qy 1 MGNDPPAVEAPPSFRSLFGLDLKISPVAPDADAVAAQILSLPLKFF-PIIVIGIIAL 59  
Db 1 MGNDPPAVEAPPSFRSLFGLDLKISPVAPDADAVAAQILSLPLPEVFSQSSSLGIIAL 60  
Qy 60 ILALAIGLGHFDCSGKRCRSSFCKIELTARCDGVSDCKDGEYRCVVRGQNAVLOV 119  
Db 61 ILALAIGLGHFDCSGKRCRSSFCKIELTARCDGVSDCKDGEYRCVVRGQNAVLOV 120  
Qy 120 FTAASWKTMCSDWKGHYANVACAQLGFPSVSSDNLRVSSLEGQFREEFVSDHLLPDD 179  
Db 121 FTAASWKTMCSDWKGHYANVACAQLGFPSVSSDNLRVSSLEGQFREEFVSDHLLPDD 180  
Qy 180 KVTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNLSLLSQWPQASLOFGY 239  
Db 181 KVTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNLSLLSQWPQASLOFGY 240  
Qy 240 HLCGGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLDNDNPAPSHLVKIVHSHYKPK 285  
Db 241 HLCGGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLDNDNPAPSHLVKIVHSHYKPK 293

RESULT 4  
US-09-342-749-2  
; Sequence 2, Application US/09342749  
; Patent No. 6166194  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Alexander K.C.  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Teng, David H.-F.  
; APPLICANT: Myriad Genetics, Inc.  
; TITLE OF INVENTION: TMRPS2 is a Tumor Suppressor  
; FILE REFERENCE: 2318-202  
; CURRENT APPLICATION NUMBER: US/09/342,749  
; CURRENT FILING DATE: 1999-06-29  
; EARLIER APPLICATION NUMBER: US 60/091,044  
; EARLIER FILING DATE: 1998-06-29  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-342-749-2

Query Match 36.2%; Score 885; DB 3; Length 492;  
Best Local Similarity 46.0%; Pred. No. 1.4e-77;  
Matches 189; Conservative 53; Mismatches 149; Indels 20; Gaps 10;

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|----|-----|---|-----|
| QY | 52  | IVIGIIALLAIGUGTHF---DCSGK-YPCRSSFKCIELIARCQDGVGCKDQDEYRC      | 107 |
| Db | 89  | LTGLTGVGAALAAAGLLKFKWGSKCSNGIEDSSGTCINPSNWDGVSHCPGGEDENRC     | 148 |
| QY | 108 | VRVGQNAVQLVFTA--ASWKTMCSDMKGHYANVACAQLGFF-SYVSDNLNLRVSSLEQG   | 164 |
| Db | 149 | VLVYGFNFILQVYSQRKSWHPVCDDWNNENYGRAACRDYKXNFYSQGI VDDSGSTS     | 208 |
| QY | 165 | FREEFVSDHLLPDKVTALHHSVYVRBGCASGHVTLQCTACGHRRGYS--SRIVGGMN     | 222 |
| Db | 209 | FMKLNTSAGNV---DIYKKLYHS---DACSSKAVSLRGTACGVNLNRSROSRIYGGES    | 261 |
| QY | 223 | SLLSQWPMQASLQFGYHLCCGVSITPLWIIITAAHCY-YDLVLPKSKTIQGVLV---SLLD | 279 |
| Db | 262 | ALPGAWFQWVSUHVQNVHVCSSIIITPEWITAAHCVEKPLNHPWHTAPAGLILRSFNF    | 321 |
| QY | 280 | NPAPSLVEKIIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQVCLPNSBENFPDGKVCW   | 339 |
| Db | 322 | YGA-GYQVEKVIISHPNYSKTKNNDIALMKLQKPLTENDLVKPVCLPNGMMLPQQLCW    | 380 |
| QY | 340 | TSQGWGATEDGDASPVLNAAVPLISKNHRDVIYGGIIISPSMLCAGYITGVGVDSQGD    | 399 |
| Db | 381 | ISGWGATEEKGTSEVLNAAKVLIIETQKNSRYVYDNLITPAMICAGPLQGNVDSQGD     | 440 |
| QY | 400 | SGGPLVCQERRLWLKVGATSPFGCAEVNKPQGVTRVTSFLDWIHEQMRD             | 450 |
| Db | 441 | SGGPLVTSKNTTWIIIGDTSWGSQKAYRPGVYVNMVFTDWIYQMRAD               | 491 |

RESULT 5  
US-09-691-840-2  
Sequence 2, Application US/09691840  
Patent No. 6444419  
GENERAL INFORMATION:  
APPLICANT: Wong, Alexander K.C.  
APPLICANT: Tavcigian, Sean V.  
APPLICANT: Teng, David H.-F.  
APPLICANT: Myriad Genetics, Inc.  
TITLE OF INVENTION: Tmprs2 is a Tumor Suppressor  
FILE REFERENCE: 2318-202  
CURRENT APPLICATION NUMBER: US/09/691,840  
CURRENT FILING DATE: 2000-10-18  
PRIOR APPLICATION NUMBER: US/09/342,749  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 60/091,044  
PRIOR FILING DATE: 1998-06-29  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Hmo sapiens  
US-09-691-840-2

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262 262 ALPGAMPQVSLHVQNHHVCGSGSIITPEWTVTAAHCVCVEKPLNNPWHWTAFAGILRQSFMF 321
Qy 280 NPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTENEMIQPVCLPNSSEENFPDGKVCW 339
Db 322 YGA-GYQVEKVISHPNVDSTKKNIDIALMKLQKPLTENDLVKVPCLPSPGMMLOPEQLCW 380
Qy 340 TSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVIYGGIISPSMLCAGYLTGGVDSQCGD 399
Db 381 ISGWGATEERKGTSEVLNAAKVLIIETQRCNSRYVDNLNLTTPAMICAGFLQGNVDSQCGD 440
Qy 400 SGGPLVQCEERLMLKVGATSGFICAEVKNKPGVYTRVTSFLDNIHQMERD 450
Db 441 SGGPLVTSKNINWLLIGTSGWGGCAXAYRPGVYGNVWFDTMIYQMRAD 491

RESULT 6
US-09-685-166A-895
; Sequence 895, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 895
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-895

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; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-691-840-2

      *
      Query Match      36.2%; Score 895; DB 4; Length 492;
      Best Local Similarity 46.0%; Fred. No. 1.4e-77;
      Matches 189; Conservative 53; Mismatches 14; Indels 20; Gaps 10
      QY 52 IVIGIIALILALAIGLGIHF---DCSGK-YRCRSFKCIEIARCDGVSCDCKGDEYRC 107
      Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      89 LTLGTFLVGAALAAGLLAKFKPMGSKCSNSGIECDSSGTCINPSNWCDDGVSHCPGGEDENRC 148
      QY 108 VRVGQONAVLQVFTA--ASWKTMCSDDMKGHVYANVACAQLGPF-SYVSDDNLRVSSLEQG 164
      Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      149 VRLYGFNFILOYYSQKRSWHFVPCDDNNYVGRACRDMGYKNFYSGQIVDDSGSTS 208
      QY 165 FREEFVSIDHLPDDKKVTALHHVSVVREGCASHVVTLOCTACGHRRYVS--SRIVGGNM 222
      Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      209 FMKLNTSAGN---DIYKKLYHS----DACSSKAVVSLRCLACGVNLNSSRQSRIVGGES 261
      QY 223 SLLSQWPQWASIQFGYHLCCGGSVITPILWIIITPAACHV-YDLILPKSWITQVLV--SLLD 279
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

|     |    |   |     |
|-----|----|---|-----|
| 340 | QY | TSGWGATGGDASPVLNHAAVPLISNKICNHRDHYCGIILSPWLCAGYLTGVDSCQGD | 399 |
| 381 | Db | ISGWGATBEKGTSEVLNAAKVLIIETQRCNSRYVDNLITPAMICAGFLQGNVDSQGD | 440 |
| 400 | QY | SGGPLVCCBERRLKWLIVGATSGIGCAEVNKPQVYTRVTSFELDTHEQME        | 448 |
| 441 | Db | SGGPLVATNNINLWLIIGDTSGSGGCAKAYRPGVYGNWVTFDIIYROMK         | 489 |

## RESIST 7

```

US-09-518-046-23
; Sequence 23, Application US/09518046
; Patent No. 6294683
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 23
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: protease domain of TADG-12 (TADG12)
US-09-518-046-23

```

|                       |         |                                 |                             |            |        |      |   |
|-----------------------|---------|---------------------------------|-----------------------------|------------|--------|------|---|
| Query Match           | 35.3 %  | Score                           | 862                         | DB 3       | Length | 157  |   |
| Best Local Similarity | 100.0 % | Prod. No.                       | 4.8e-76                     |            |        |      |   |
| Matches               | 157     | Conservative                    | 0                           | Mismatches | 0      | Gaps | 0 |
| Qy                    | 250     | LMIITAAHCYDYLIPKSWTIQGVLSLLDNPA | SHLVEKIVHSHKYKPKRIGNDIALMK  | 309        |        |      |   |
| Db                    | 1       | LMIITAAHCYDYLIPKSWTIQGVLSLLDNPA | SHLVEKIVHSHKYKPKRIGNDIALMK  | 60         |        |      |   |
| Qy                    | 310     | LAGPLTFNEMIQVCLPNSSENFDPDGKVCW  | TSGWATEDGGDASPVLNHAAPVLSNKC | 369        |        |      |   |
| Db                    | 61      | LAGPLTFNEMIQVCLPNSSENFDPDGKVCW  | TSGWATEDGGDASPVLNHAAPVLSNKC | 120        |        |      |   |
| Qy                    | 370     | NHRDYYGGIISPSMLCAGYLTCGVDS      | CGGSGGPLVC                  | 406        |        |      |   |
| Db                    | 121     | NHRDYYGGIISPSMLCAGYLTCGVDS      | CGGSGGPLVC                  | 157        |        |      |   |

## RESULT 8

```

US-08-807-151-1
; Sequence 1, Application US/08807151
; Patent No. 6043033
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSO Version 2.0

```

## RESULT 9

US-09-478-957-1  
Sequence 1, Application US/09478957  
Patent No. 6350448  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Lal, Preeti  
TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED  
TITLE OF INVENTION: PROTEASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:

```
/ APPLICATION NUMBER: US/09/478,957
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/807,151
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0227 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 283 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: SCORNOT01
/ CLONE: 556016
/ US-09-478-957-1

Query Match      28.5%; Score 696; DB 4; Length 283;
Best Local Similarity 50.4%; Pred. No. 1.6e-59;
Matches 137; Conservative 37; Mismatches 92; Indels 6; Gaps 4;

QY 184 LHSVYVREGCASHGVVTTQCTACGHRGYS--SRIVGNGMSSLQWPQASLQCGYHL 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 IYKLYSDACSSKAVVSLRCLACGYNLSRQSRIVGSGESALPGAWPQVSLRVQNVHV 71

QY 242 CGGSVITPLWITTAACHV-YDLVLPKSWTIQGLV--SLLDNPAHPSHLVEKIVYHSKYK 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 CGGSITPEWITVAACHVEKPLNPNWHWTAAGILRQSFNFYGA-GYQKRVISHPNVD 130

QY 299 KRLGNDIALMKLAGPLTFNEMIQVCLPNSEENFPDGKVCWTSGWAGEDGSDGAPVLNH 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 KTKNDIALMKLQKPLTFNDLVKPCVCLPNPMMQLQPEQLCWTSGWATEBKGTSEVLNA 190

QY 359 AAVPLISNKTCHRDVYGGIISPMCLAGVLTGVDSCOGSDGGPLAVCOERLKLVGAT 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 AKVLLIETQCNRYVYDNLITPAMICAGFLQGNVDSCOGSDGGKLVTSKNINWMLIGDT 250

QY 419 SFGIGCAEVNKPVGVTYRTVSFLDWIHEQMERD 450
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 251 SWSGCAKAYRPGVYGNVYFTDWIYRQMEAD 282

RESULT 10
US-09-820-002-4
; Sequence 4, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu
; APPLICANT: Ye, Jane
; APPLICANT: Difrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: HUMAN
/ US-09-820-002-4

Query Match      27.6%; Score 674; DB 4; Length 417;
```

```
Best Local Similarity 35.8%; Pred. No. 3.8e-57;
Matches 149; Conservative 62; Mismatches 143; Indels 62; Gaps 11;

QY 59 LIALALAIIGLHFDPCGKYRCRSFXCIELIARCDGVSDCKDGEDBYRCVRYGGQNAVLIQ 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 LILLTAIG-----AASWAIVAVLLRSD-----QEPLYPVQVSSADARLM 64

QY 119 VF--TAASWTKMCSDDWKGHYANVACAQIGFSPYVSSDNLRYSSLSGQFRERFVSDHLL 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 VFDKTEGTWLLCSSRNARVAGLSCEMGFURALTHSELDTAGANGTSGFFCVDE-- 122

QY 177 PDDKVTALHSHSVYVRE-----GCASGHVVTLOCTACGHRGYSRRIVGNGMSSLQWPQ 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 -----GELPHTQRLLEVISFSDCPRGRFLAAICQDCGRRLKLPVDRIVGGRDTSLGRWPWQ 177

QY 232 ASLQFQGYHLGGSVITPLWITTAACHVVDLYLPK-----SWTIQVGLVSLLDNAPSH 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 VSLRYDGAHLGGSLLSGDMVLTAAHC-----FPERNRVLSRVRVFAVA-----QASPHG 229

QY 286 L---VEKIVYHSKYKPKR-----LGNIDIALMKLAGPLTFNEMIQVCLPNSEENFPDGK 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 LQLGQAVVYHGGYLPFRDPNSEENSDIALVHLSPLPLTEYIQVCLPAAGCALVDGK 289

QY 337 VCVTSGWATEDGGDASPVLNHAAPVLISNKNINHRDVTGGIISPSMLCAGYLTGGVDS 396
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 ICTVTGNGNTQYIGQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDAC 349

QY 397 QGDSGGPLVCOE---RRLMKLVGATSGIGCAEVNKPVGVTYRTVSFLDWIHEQME 448
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 350 QGDSGGPFVCEDSISRTPRWRLCGIVSGVGTGALCAQKPGVYTKVSDFERWIFQAIK 405

RESULT 11
US-08-200-900A-2
; Sequence 2, Application US/08200900A
; Patent No. 5665566
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,900A
; FILING DATE: 23-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, Maureen C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5201-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170 X8574
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
/ US-08-200-900A-2

Query Match      27.4%; Score 669.5; DB 1; Length 798;
```

[illegible]

|  |     |  |     |
|--|-----|--|-----|
| Qy   | 234 | LQFGYHLCCGGSVITPLWITTAACHCYVDLYL--PKSWTIQVGL--VSLLDNP-APSHLVEK | 289 |
| Db   | 581 | LYFDDQVCAGASVSDWLVSAAHCVYGRNWPESKRWAVLGLHMASLNTSPQIETIRLDQ     | 640 |
| Qy   | 290 | IVVESHKPKRLGNDIALMKLAGPLTFNEMIQVCLPNSPENFPDQKVCWTSGMGATEDG     | 349 |
| Db   | 641 | IVINPHYNKERKNDIAMWHELMKVNYTDYIQICLPEENQVFPFPGRICSIAGWGALIYQ    | 700 |
| Qy   | 350 | GDASPVLNHAAVPLISNKINCHR-DVYGGHISPMICAGYLTGGVDSQGDGSGGPLYCOE    | 408 |
| Db   | 701 | GSTADVLQEAADVPLLSNEKCCQQQMPEN--ITENMVCAGYEAAGGVDSQGDGSGPLMCOE  | 758 |
| Qy   | 409 | RRLWKLVGATSGIGCAEVNKPGVYTRVTSFLDWI                             | 443 |
| Db   | 759 | NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTW                              | 793 |
| RESULT 13  |     |  |     |
| US-09-656-002-2  |     |  |     |
| ; Sequence 2, Application US/09656002  |     |  |     |
| ; Patent No. 6455668   |     |  |     |
| ; GENERAL INFORMATION:   |     |  |     |
| ; APPLICANT: Mack, Kurt  |     |  |     |
| ; APPLICANT: Gish, Kurt  |     |  |     |
| ; APPLICANT: Wilson, Keith   |     |  |     |
| ; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITI |     |  |     |
| ; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS            |     |  |     |
| ; FILE REFERENCE: A-69108/DJB/JJD/AMS  |     |  |     |
| ; CURRENT APPLICATION NUMBER: US/09/656,002                                    |     |  |     |
| ; CURRENT FILING DATE: 2000-09-06  |     |  |     |
| ; PRIOR APPLICATION NUMBER: US 09/525,993                                      |     |  |     |
| ; PRIOR FILING DATE: 2000-03-15  |     |  |     |
| ; PRIOR APPLICATION NUMBER: US 09/493,444                                      |     |  |     |
| ; PRIOR FILING DATE: 2000-01-28  |     |  |     |
| ; PRIOR APPLICATION NUMBER: PCT/US 00/07044                                    |     |  |     |
| ; PRIOR FILING DATE: 2000-03-15  |     |  |     |
| ; NUMBER OF SEQ ID NOS: 3  |     |  |     |
| ; SOFTWARE: Patent in version 3.0  |     |  |     |
| ; SEQ ID NO 2  |     |  |     |
| ; LENGTH: 423  |     |  |     |
| ; TYPE: PRT  |     |  |     |
| ; ORGANISM: Homo sapiens   |     |  |     |
| US-09-656-002-2  |     |  |     |
| Query Match 27.2%; Score 665.5; DB 4; Length 423;                              |     |  |     |
| Best Local Similarity 35.4%; Pred. No. 2.6e-56;                                |     |  |     |
| Matches 160; Conservative 72; Mismatches 157; Indels 63; Gaps 16;              |     |  |     |
| Qy   | 26  | ISPVPADADAVAQAIIISLLPLKFPPIVIGIIALIL--ALAIGLGHFDCSGKYRCRSS     | 82  |
| Db   | 9   | VSPWRPSESVGPIPLIIALLSLAI--IIIVVLIRKILDYVFLCCQPLHF              | 56  |
| Qy   | 83  | FKCIELIARCDGVSDCKDGDGDEYRC-----VRVGGQNNAVQLVFTAA--SWKTC        | 129 |
| Db   | 57  | --IPRQLCDGELDCPLIGEDDEHCVKSPFEGPAVAVRLSKDRSTLQVLDSATGNWFSAC    | 113 |
| Qy   | 130 | SDWKGHYANVACAQLGFPSPVSSDNLRVSLGECQFEEFVSIIDHLLPDDKVVALHSHVY    | 189 |
| Db   | 114 | FDNFEALAEACACQMGYSS-----KPTFRAVEIGPDQDLVDVVEITENSQELR          | 161 |
| Qy   | 190 | VREG--CASHGVVTLQCTACGHRRGYSSRIIVGNMILLSQWPQASLQFQGYHLCCGSV     | 246 |
| Db   | 162 | MENSSGCLSGSLVSLHCLACG-KSLXTPRVVGGEASVDSWPMQVSIQYDKQHVCGGSI     | 220 |
| Qy   | 247 | ITPLWITTAHCV---VDLYLPKSWTQTVGLVSLLDNPAFPHLVEKIV---YHSKYKPKR    | 300 |
| Db   | 221 | LDPHWLTAACHCFRKHDTDFV---NWKVRAGSDKL--GSFPLAVAKIIIEFNPMY-PK-    | 273 |
| Qy   | 301 | LGNDIALMKLAGPLTFNEMIQVCLPNSPENFPDQKVCWTSGMGAT-EDGGDASPLNHA     | 359 |
| Db   | 274 | -DNIALMKLQPLTFSGTRVPICLPFDDEELTATPLWIIIGWGTQKGGKWSDILLQA       | 332 |
| Qy   | 360 | AVPLISNKINHRDVIYGGIISPSMLCAGYLTGGVDSQGDGSGGPLVCCOERIWNKLUGATS  | 419 |

Db 333 SVQVISTRCNADDAVQGEVTEKMCAGIPEGGVDTCQDGGPLMYQSDQ-WHVVGIVS 391  
Qy 420 FGIGCAEVNKPQVYTRVTSFLDWIHEQMERDL 451  
Db 392 WGVGCGGSPSPGVYTKVSAVYLNWYVWKAEL 423  
RESULT 14  
US-09-000-846-2  
; Sequence 2, Application US/09000846  
; Patent No. 5981830  
; GENERAL INFORMATION:  
; APPLICANT: WU, QINGYU  
; TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH  
; TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
; STREET: 2200 CLARENDON BLVD. SUITE 1400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/000,846  
; FILING DATE: 30-DEC-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/866,058  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEBOVITZ, RICHARD M.  
; REGISTRATION NUMBER: 37,067  
; REFERENCE/DOCKET NUMBER: BERL 65P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-243-6333  
; TELEFAX: 703-243-6410  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 416 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-000-846-2  
Query Match 27.2%; Score 665; DB 2; Length 416;  
Best Local Similarity 38.1%; Pred. No. 2.9e-56;  
Matches 143; Conservative 54; Mismatches 136; Indels 42; Gaps 9;  
Qy 100 DGEDEYRCVRVGGQNAVLOVF--TAAASKWTCSDDKWGHYANVACAGLGPSPVSSDNL 157  
Db 46 DQEPYIQ-VQLSPGDSRLAVFDKTEGTWLLCSRSRNARVAGLCEEMGFLRALHSEL 104  
Qy 158 VSSLEGQFRFEFVSID-----HLLPDDKVTALHHSVYVRESCASGHVYVTLQCTACGH 209  
Db 105 VRTAGANGTSGFFCVDEGLRLAQRLL--DVISVC-----DCPRGRLTATCQDCGR 154  
Qy 210 RRGVSSRIVGNMILLQWPHQASLOPQGVHLCGSGVITPLWITAHCVYDIYLPK--- 266  
Db 155 RKLFPVDRIVGGQDSSLGRWPQVSLRYDGTGHLCCGSLLSGDWLVTAHC-----FFERNR 209  
Qy 267 ---SWTIQVGLVLLDNPAPSHLVKEIVYHSKYKPKR-----LGNDIALMKLAGPJTEN 317  
Db 210 VLSRWRVFAVARTSPHVLQGVQAVIYHGGYLPFRDPIDENSDIALVHLSLSPLT 269  
Qy 318 EMIQVCLPNSSENPDPCKVCWTSNGATEDGGDASPVLNHAAPVLISNKNHRDVIYG 377

Db 270 EYIQPVCLPAAQALVDKQVCTVTKWNTQFYGGQNAVLOVEARVPIISNEVCNSPDPYGN 329  
Qy 378 IISFMSLCAGYLTGVDSCQDGGPLVCQB-----RELWKLVGATSGIGCAEVNKPQVY 433  
Db 330 QIKPKMFCAGYPEGIDACQDGGPFCVCDTSISGTSRWLCLGIVSWGTCALARKPGVY 389  
Qy 434 TRVTSFLDWIHEQME 448  
Db 390 TKVTDFFREWIFRAIK 404  
RESULT 15  
US-09-008-271A-6  
; Sequence 6, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,271A  
; FILING DATE: 16-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mohan-Peterson, Sheela  
; REGISTRATION NUMBER: 41,201  
; REFERENCE/DOCKET NUMBER: PF-0458 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 435 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: COLNNOT13  
; CLONE: 1337018  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :  
US-09-008-271A-6  
Query Match 26.9%; Score 658; DB 3; Length 435;  
Best Local Similarity 35.7%; Pred. No. 1.5e-55;  
Matches 158; Conservative 74; Mismatches 147; Indels 64; Gaps 18;  
Qy 44 LPLKFPPIVIGIILAIILALA-----TGLGHFDCSKYRCRSFKC---IELIAR--- 91  
Db 22 IPMETFRKVGPIIALLSLASIIIVVLIKVID---KY---YFLCGQPLHFTPRKOL 74  
Qy 92 CDGVSDCKDGEDEYEC-----VRVGGQNAVLOVFTAA--SWKTCSDDKWGHYA 138

Db 75 CDGELDCPLGEDEHCVKFFPEGPAVAVLRSKDRSTLQVLDSATGNWFSACFDNFTEALA 134  
QY 139 NVACAQLGFPSPYVSSDNLRVSSLEGGFREEFVSIHLLPDDKVTALHHSVYVREG---CA 195  
Db 135 ETACRQWGYSS-----KPTFRAVEICPDQDLDVVEITENSQELRMENSSGPCL 182  
QY 196 SGHVTLQCTACGHRGYSRIVGGMNLSLLSQWPQASLQFQYHLCGGSVITPLWITA 255  
Db 183 SGLSVSLHCLACGESL-KTPRVVGGEEASVDSWPFQVSIQYDKQHVCGGSILDPHWLTA 241  
QY 256 AHCV---YDLYLPKSWTIQVGLVSLLDNPAFSLHVEKIV---YHSKYKPKRLGNDIALMK 309  
Db 242 AHCFRKHDTVF---NWKVRAGSKL--GSFPFLAVAKIIIBFNPMY-PK--DNDIALMK 293  
QY 310 LAGPLTFNEMIQVCLPNSBEENFPDGKVCWTSWGAT-EDGGDASPVLNHAAVPLISNKI 368  
Db 294 LQPLTFSGTVRPICLFFFEDEELTPATPLMIIIGWFTKONGGKMSDILLQASVQVIDSTR 353  
QY 369 CNHRDVYGGIISPSMLCAGYLTGGVDSGQDSGGPLVCOERRLWKLVGATSFIGIGCAEVN 428  
Db 354 CNADDAVQGEVTEKMMKAGIPEGGVTCQDSGGPLMYQSDQ-WHVVGIVSWNGYCGGSPS 412  
QY 429 KPGVYTRVTSFLDWIHEQMERDL 451  
Db 413 TPGVYTKVSAYLNNWYNNVWKAEL 435

Search completed: May 5, 2004, 15:49:26  
Job time : 23 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:48:26 ; Search time 47 Seconds  
(without alignments)

2671.636 Million cell updates/sec

Title: US-09-846-512-2

Perfect score: 2443

Sequence: 1 MGENDPPAVEAPFRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189591 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
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| 2          | 2443  | 100.0       | 453    | 9  | US-09-978-637-69  |
| 3          | 2443  | 100.0       | 453    | 9  | US-09-978-192A-69 |
| 4          | 2443  | 100.0       | 453    | 9  | US-09-999-832A-69 |
| 5          | 2443  | 100.0       | 453    | 10 | US-09-978-189-69  |
| 6          | 2443  | 100.0       | 453    | 10 | US-09-978-608A-69 |
| 7          | 2443  | 100.0       | 453    | 10 | US-09-978-585A-69 |
| 8          | 2443  | 100.0       | 453    | 10 | US-09-978-191A-69 |
| 9          | 2443  | 100.0       | 453    | 10 | US-09-978-403A-69 |
| 10         | 2443  | 100.0       | 453    | 10 | US-09-978-564A-69 |
| 11         | 2443  | 100.0       | 453    | 10 | US-09-999-833A-69 |
| 12         | 2443  | 100.0       | 453    | 10 | US-09-981-915A-69 |
| 13         | 2443  | 100.0       | 453    | 10 | US-09-978-824-69  |
| 14         | 2443  | 100.0       | 453    | 10 | US-09-918-585A-69 |
| 15         | 2443  | 100.0       | 453    | 10 | US-09-978-423A-69 |

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| 19 | 2443 | 100.0 | 453 | 10 | US-09-978-187B-69 |
| 20 | 2443 | 100.0 | 453 | 10 | US-09-978-643A-69 |
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| 22 | 2443 | 100.0 | 453 | 10 | US-09-978-375A-69 |
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| 25 | 2443 | 100.0 | 453 | 10 | US-09-978-681A-69 |
| 26 | 2443 | 100.0 | 453 | 10 | US-09-978-194A-69 |
| 27 | 2443 | 100.0 | 453 | 10 | US-09-999-829A-69 |
| 28 | 2443 | 100.0 | 453 | 10 | US-09-978-239A-69 |
| 29 | 2443 | 100.0 | 453 | 10 | US-09-978-544A-69 |
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| 31 | 2443 | 100.0 | 453 | 10 | US-09-978-802A-69 |
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| 36 | 2443 | 100.0 | 453 | 12 | US-10-201-858-64  |
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| 39 | 2443 | 100.0 | 453 | 12 | US-10-208-024-64  |
| 40 | 2443 | 100.0 | 453 | 12 | US-10-201-853-64  |
| 41 | 2443 | 100.0 | 453 | 12 | US-10-013-917A-69 |
| 42 | 2443 | 100.0 | 453 | 12 | US-10-174-581-64  |
| 43 | 2443 | 100.0 | 453 | 12 | US-10-176-483-64  |
| 44 | 2443 | 100.0 | 453 | 12 | US-10-176-749-64  |
| 45 | 2443 | 100.0 | 453 | 12 | US-10-176-914-64  |

#### ALIGNMENTS

#### RESULT 1

US-09-978-295A-69

; Sequence 69, Application US/09978295A

; Patent No. US20020156006A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC11

; CURRENT APPLICATION NUMBER: US/09/978,295A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

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|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGENDPVAEAPFERSFGUDDUKISPVADADAAQAQLSLPLKFFPIIVIGIIALI 60
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DB 61 LALAIGLGIHFDGSKYRCRSFXCIELIARCDGVSDCKGDEYRCVVRGGQNAVLOVF 120
QY 121 TAASKWTCSDDKWGHYANVACAQLGFPYSYSSNLRVSLLEGQFREFFVSIDHLLPDDK 180
DB 121 TAASKWTCSDDKWGHYANVACAQLGFPYSYSSNLRVSLLEGQFREFFVSIDHLLPDDK 180
QY 181 VTALHSHVYVEEGCASGHVVTLOCTACGHRGYSRIVGNNMSSLQWPMQASLQFQGYH 240
DB 181 VTALHSHVYVEEGCASGHVVTLOCTACGHRGYSRIVGNNMSSLQWPMQASLQFQGYH 240
QY 241 LCGSVITPLMIITAAHCYVDLXLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKR 300
DB 241 LCGSVITPLMIITAAHCYVDLXLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKR 300
QY 301 LGNDIALMKLAGPLTFNEMIQVCLPNSSEENFPDGKVCWTSWGAATEDGGDASPVLNHAA 360
DB 301 LGNDIALMKLAGPLTFNEMIQVCLPNSSEENFPDGKVCWTSWGAATEDGGDASPVLNHAA 360
QY 361 VPLISNKCINHRDVGIIISPSMLCAGYLTGGVDSQQDGGPLVCQERLWKLVGATSF 420
DB 361 VPLISNKCINHRDVGIIISPSMLCAGYLTGGVDSQQDGGPLVCQERLWKLVGATSF 420
QY 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453
DB 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453

RESULT 2

US-09-978-697-69
; Sequence 69, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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;; PRIOR APPLICATION NUMBER: 60/085697

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Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 GIGCAEWKPGVYTRVTSFLDWIHQMERDLKT 453

RESULT 3

US-09-978-192A-69

Sequence 69, Application US/09978192A

Patent No. US20020177553A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

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APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C9

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CURRENT FILING DATE: 2001-10-15

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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Wood, William I.
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TITLE OF INVENTION: Acids Encoding the Same
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| 41 | PRIOR FILING DATE: 1998-03-31       |  |
| 42 | PRIOR APPLICATION NUMBER: 60/080165 |  |
| 43 | PRIOR FILING DATE: 1998-03-31       |  |
| 44 | PRIOR APPLICATION NUMBER: 60/080194 |  |
| 45 | PRIOR FILING DATE: 1998-03-31       |  |
| 46 | PRIOR APPLICATION NUMBER: 60/080334 |  |
| 47 | PRIOR FILING DATE: 1998-04-01       |  |
| 48 | PRIOR APPLICATION NUMBER: 60/081070 |  |
| 49 | PRIOR FILING DATE: 1998-04-01       |  |
| 50 | PRIOR APPLICATION NUMBER: 60/080328 |  |
| 51 | PRIOR FILING DATE: 1998-04-01       |  |
| 52 | PRIOR APPLICATION NUMBER: 60/080333 |  |
| 53 | PRIOR FILING DATE: 1998-04-01       |  |
| 54 | PRIOR APPLICATION NUMBER: 60/081071 |  |
| 55 | PRIOR FILING DATE: 1998-04-08       |  |
| 56 | PRIOR APPLICATION NUMBER: 60/081195 |  |
| 57 | PRIOR FILING DATE: 1998-04-08       |  |
| 58 | PRIOR APPLICATION NUMBER: 60/081203 |  |
| 59 | PRIOR FILING DATE: 1998-04-09       |  |
| 60 | PRIOR APPLICATION NUMBER: 60/081239 |  |
| 61 | PRIOR FILING DATE: 1998-04-09       |  |
| 62 | PRIOR APPLICATION NUMBER: 60/081955 |  |
| 63 | PRIOR FILING DATE: 1998-04-15       |  |
| 64 | PRIOR APPLICATION NUMBER: 60/081817 |  |
| 65 | PRIOR FILING DATE: 1998-04-15       |  |
| 66 | PRIOR APPLICATION NUMBER: 60/081819 |  |
| 67 | PRIOR FILING DATE: 1998-04-15       |  |
| 68 | PRIOR APPLICATION NUMBER: 60/081952 |  |
| 69 | PRIOR FILING DATE: 1998-04-15       |  |
| 70 | PRIOR APPLICATION NUMBER: 60/081952 |  |

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 2443; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGENPPAVEAPFSPRSLEGLDOLKTSVPADADAVAAQILSLLEPKFFPIIVIGIILI 60
Db 1 MGENPPAVEAPFSPRSLEGLDOLKTSVPADADAVAAQILSLLEPKFFPIIVIGIILI 60
QY 61 LALAIGLGHFDCSGKYRCRSFKCIELIARCDGVSDCKGDEYRCVVRVGQNAVLOVF 120
Db 61 LALAIGLGHFDCSGKYRCRSFKCIELIARCDGVSDCKGDEYRCVVRVGQNAVLOVF 120
QY 121 TAASWTKMCDWKGHYANVACAQLGFPYSVSSDNLRVSSLEGOFRBEFVSIDHLLPDK 180
Db 121 TAASWTKMCDWKGHYANVACAQLGFPYSVSSDNLRVSSLEGOFRBEFVSIDHLLPDK 180
QY 181 VTALHSHVVRREGCASHGVVTLQCTACGHRGYSRIVGNNMSLLSQWPQASLQFGYH 240
Db 181 VTALHSHVVRREGCASHGVVTLQCTACGHRGYSRIVGNNMSLLSQWPQASLQFGYH 240
QY 241 LCGSVITPLWITTAACHVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVVHSHYKPKR 300
Db 241 LCGSVITPLWITTAACHVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVVHSHYKPKR 300
QY 301 LGNDIALMKLAGLPTNEMIQVCLPNSNENPDGKVCWTSGWATEDGGDASPVLNAA 360
Db 301 LGNDIALMKLAGLPTNEMIQVCLPNSNENPDGKVCWTSGWATEDGGDASPVLNAA 360
QY 361 VPLISKNICNHRDVGIIISPSMLCAGYLTGGVDSQCGSGGLVCQERRLKVLGATSP 420
Db 361 VPLISKNICNHRDVGIIISPSMLCAGYLTGGVDSQCGSGGLVCQERRLKVLGATSP 420
QY 421 GIGCAEVNKGVTYRTVTSFLDWIHEQWERDLKT 453
Db 421 GIGCAEVNKGVTYRTVTSFLDWIHEQWERDLKT 453

RESULT 5
US-09-978-189-69
; Sequence 69, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
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; PRIOR APPLICATION NUMBER: 60/081049
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; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR APPLICATION NUMBER: 60/081817
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225; Indels 0; Gaps 0;
Matches 453; Conservative 0; Mismatches 0;

QY 1 MGENDPPEAVEAPFSPRSLFGLDDDLKISVPADADAAVAQAIIISLLPLKFFPIIVIGIIALI 60
DB 1 MGENDPPEAVEAPFSPRSLFGLDDDLKISVPADADAAVAQAIIISLLPLKFFPIIVIGIIALI 60
QY 61 LALAIGLGHFDCSGKYRCRSFKCIELIARCDGVSDCKDGEDYRCVVGQNAVLOVF 120
DB 61 LALAIGLGHFDCSGKYRCRSFKCIELIARCDGVSDCKDGEDYRCVVGQNAVLOVF 120
QY 121 TAASWKTMCSDWKGHYANVACAQLGFFSYVSSDNLRVSSLEGQFREFVSIIDHLLPDK 180
DB 121 TAASWKTMCSDWKGHYANVACAQLGFFSYVSSDNLRVSSLEGQFREFVSIIDHLLPDK 180
QY 181 VTALHSHVYVREGCASGHVVTILQCTACGHRRGYSRIVGGNNMSSLLOPWFQASLOFQGYH 240
DB 181 VTALHSHVYVREGCASGHVVTILQCTACGHRRGYSRIVGGNNMSSLLOPWFQASLOFQGYH 240
QY 241 LCGSVITPLWITTAHCYVDLYLPKSWTIOVGLVSLLDNPAHPSHLVEKIVVHSHYKPKR 300
DB 241 LCGSVITPLWITTAHCYVDLYLPKSWTIOVGLVSLLDNPAHPSHLVEKIVVHSHYKPKR 300
QY 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSSEENPPDGKVCWTSWGATEGGDASPVLNHA 360
DB 301 LGNDIALMKLAGPLTFNEMIQPVCLPNSSEENPPDGKVCWTSWGATEGGDASPVLNHA 360
QY 361 VPLISNKICNHRDGVYGGIISPSMLCAGYLTGVSDSCQDGGPLVCQERRLKLVGATSF 420
DB 361 VPLISNKICNHRDGVYGGIISPSMLCAGYLTGVSDSCQDGGPLVCQERRLKLVGATSF 420
QY 421 GIGCAEVNKPVGVTYTRVTSFLDWIHEQMERDLKT 453
DB 421 GIGCAEVNKPVGVTYTRVTSFLDWIHEQMERDLKT 453

RESULT 6
US-09-978-608A-69
; Sequence 69, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
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APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P26301C22  
CURRENT APPLICATION NUMBER: US/09/978,608A  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 69  
LENGTH: 453  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-608A-69

Query Match 100.0%; Score 2443; DB 10; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.3e-225;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGENDPPAVEAPFSRSLFGLDLDKISPVADADAVAAQILSLPLKFFPIIVIGIILI 60  
DB 1 MGENDPPAVEAPFSRSLFGLDLDKISPVADADAVAAQILSLPLKFFPIIVIGIILI 60

QY 61 LALAIGLGHFDCSGKYRCRSSFKCIELIARCDGVSDDCKDGEDEYRCVVGQNAVLOVP 120  
DB 61 LALAIGLGHFDCSGKYRCRSSFKCIELIARCDGVSDDCKDGEDEYRCVVGQNAVLOVP 120

QY 121 TAASWTKMCSDDWKGHYANVACQAQLGFPVSVDNLRVSSLEGGQPREFVSIIDHLLPDDK 180  
DB 121 TAASWTKMCSDDWKGHYANVACQAQLGFPVSVDNLRVSSLEGGQPREFVSIIDHLLPDDK 180

QY 181 VTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNMSSLSSQWPQASLOFGYH 240  
DB 181 VTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNMSSLSSQWPQASLOFGYH 240

QY 241 LCGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLLDNPAFSLHVEKIVHSHKPKR 300  
DB 241 LCGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLLDNPAFSLHVEKIVHSHKPKR 300

QY 301 LGNDIALMKLAGPLTFNEMIQVCLPNSBENFPDGKVCWTSWGATEDGCDASPVLNHAA 360  
DB 301 LGNDIALMKLAGPLTFNEMIQVCLPNSBENFPDGKVCWTSWGATEDGCDASPVLNHAA 360

QY 361 VPLISNKICNHRDVGGLISPSMLCAGYLTGGVDSGGSGGLVCOERLWKLVGATSF 420  
DB 361 VPLISNKICNHRDVGGLISPSMLCAGYLTGGVDSGGSGGLVCOERLWKLVGATSF 420

QY 421 GIGCAEVNKPVGVTYRTVTSFLDWIHEQMERDLKT 453

DB 421 GIGCAEVNKPVGVTYRTVTSFLDWIHEQMERDLKT 453

RESULT 7  
US-09-978-585A-69  
Sequence 69, Application US/09978585A  
Publication No. US20030049633A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P26301C15  
CURRENT APPLICATION NUMBER: US/09/978,585A  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 69  
LENGTH: 453  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-585A-69

Query Match 100.0%; Score 2443; DB 10; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.3e-225;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGENDPPAVEAPFSRSLFGLDLDKISPVADADAVAAQILSLPLKFFPIIVIGIILI 60  
DB 1 MGENDPPAVEAPFSRSLFGLDLDKISPVADADAVAAQILSLPLKFFPIIVIGIILI 60

QY 61 LALAIGLGHFDCSGKYRCRSSFKCIELIARCDGVSDDCKDGEDEYRCVVGQNAVLOVP 120  
DB 61 LALAIGLGHFDCSGKYRCRSSFKCIELIARCDGVSDDCKDGEDEYRCVVGQNAVLOVP 120

QY 121 TAASWTKMCSDDWKGHYANVACQAQLGFPVSVDNLRVSSLEGGQPREFVSIIDHLLPDDK 180  
DB 121 TAASWTKMCSDDWKGHYANVACQAQLGFPVSVDNLRVSSLEGGQPREFVSIIDHLLPDDK 180

QY 181 VTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNMSSLSSQWPQASLOFGYH 240  
DB 181 VTALHSHVYVREGCASHGVVTLQCTACGHRGYSRIVGNNMSSLSSQWPQASLOFGYH 240

QY 241 LCGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLLDNPAFSLHVEKIVHSHKPKR 300  
DB 241 LCGSVITPLWITTAACHVVDLYLPKSWTIQVGLVSLLDNPAFSLHVEKIVHSHKPKR 300

QY 301 LGNDIALMKLAGPLTFNEMIQVCLPNSBENFPDGKVCWTSWGATEDGCDASPVLNHAA 360

Db 301 LGNDIALMKTAGLTTNEMIQPCLPNSSENFDPKGVKVTSGWGATEDGGDASPVLNHAA 360  
QY 361 VPLISNKICNHRDVGIIISPSMLCAGYLTGGVDSQSGGSLVQCERRLWKLVGATSF 420  
Db 361 VPLISNKICNHRDVGIIISPSMLCAGYLTGGVDSQSGGSLVQCERRLWKLVGATSF 420  
QY 421 GIGCAEVNKGVTYTRVTSFLDWTHEQWERDLKT 453  
Db 421 GIGCAEVNKGVTYTRVTSFLDWTHEQWERDLKT 453

RESULT 8  
US-09-978-191A-69  
; Sequence 69, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Borstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C4  
; CURRENT APPLICATION NUMBER: US/09/978,191A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585+  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
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1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.3e-225;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGENDPFAVEAPFSSRSLFGLDDDKISPVAPDADAAQIILSLPLKFFPIIVIGIIALI 60  
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DB 61 LALAIGLGHFDGSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVAVGGONAVLQVF 120  
QY 121 TAASWKTMCSDDDWKGHYANVACAQLGFPSPVSSDNLRVSLSEGOQFREFVSIIDHLLPDDK 180  
DB 121 TAASWKTMCSDDDWKGHYANVACAQLGFPSPVSSDNLRVSLSEGOQFREFVSIIDHLLPDDK 180  
QY 181 VTALHSHVYREGCASGHVVTLOCTACGHRGYSRIVGNMSSLQWPMQASLQFGYH 240  
DB 181 VTALHSHVYREGCASGHVVTLOCTACGHRGYSRIVGNMSSLQWPMQASLQFGYH 240  
QY 241 LCGGSVITPLWIIITAAHCVVYDLYLPKSWITQVGLVSLLDNPAFSLHVEKIVYHSKYKPKR 300  
DB 241 LCGGSVITPLWIIITAAHCVVYDLYLPKSWITQVGLVSLLDNPAFSLHVEKIVYHSKYKPKR 300  
QY 301 LGNDIALMKLAGPLTFNEMIQVCLPNSSENFPGKVCWTSGMGATEDGGDASPVLNHAA 360  
DB 301 LGNDIALMKLAGPLTFNEMIQVCLPNSSENFPGKVCWTSGMGATEDGGDASPVLNHAA 360  
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RESULT 9

US-09-978-403A-69  
; Sequence 69, Application US/09978403A  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
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; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
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; APPLICANT: Shelton, David L.  
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; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2,3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNDPPAVEAPSFRLGLDLDKISPVAPDADAAVAQAQILSLPLKFPPIIVIGIIALI 60
Db 1 MGNDPPAVEAPSFRLGLDLDKISPVAPDADAAVAQAQILSLPLKFPPIIVIGIIALI 60
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Qy 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453
Db 421 GIGCAEVNKPQVYTRVTSFLDWIHEQMERDLKT 453

RESULT 10
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; Sequence 69, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;

Best Local Similarity 100.0%; Pred. No. 2.3e-225; Indels 0; Gaps 0;

Matches 453; Conservative 0; Mismatches 0;

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## RESULT 11

US-09-999-833A-69  
 ; Sequence 69, Application US/09999833A  
 ; Publication No. US20030054405A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Fertara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
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 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kiljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C65  
 ; CURRENT APPLICATION NUMBER: US/09/999,833A  
 ; CURRENT FILING DATE: 2001-10-24  
 ; PRIOR APPLICATION NUMBER: 09/918595  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
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US-09-981-915A-69  
; Sequence 69, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
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; APPLICANT: Tumas, Daniel  
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| 35  | PRIOR APPLICATION NUMBER: 60/079294 | 36  | PRIOR FILING DATE: 1998-04-28       |
| 37  | PRIOR FILING DATE: 1998-03-25       | 38  | PRIOR APPLICATION NUMBER: 60/083392 |
| 39  | PRIOR APPLICATION NUMBER: 60/079656 | 40  | PRIOR FILING DATE: 1998-04-29       |
| 41  | PRIOR FILING DATE: 1998-03-26       | 42  | PRIOR APPLICATION NUMBER: 60/083495 |
| 43  | PRIOR APPLICATION NUMBER: 60/079664 | 44  | PRIOR FILING DATE: 1998-04-29       |
| 45  | PRIOR FILING DATE: 1998-03-27       | 46  | PRIOR APPLICATION NUMBER: 60/083496 |
| 47  | PRIOR APPLICATION NUMBER: 60/079689 | 48  | PRIOR FILING DATE: 1998-04-29       |
| 49  | PRIOR FILING DATE: 1998-03-27       | 50  | PRIOR APPLICATION NUMBER: 60/083499 |
| 51  | PRIOR APPLICATION NUMBER: 60/079663 | 52  | PRIOR FILING DATE: 1998-04-29       |
| 53  | PRIOR FILING DATE: 1998-03-27       | 54  | PRIOR APPLICATION NUMBER: 60/083545 |
| 55  | PRIOR APPLICATION NUMBER: 60/079728 | 56  | PRIOR FILING DATE: 1998-04-29       |
| 57  | PRIOR FILING DATE: 1998-03-27       | 58  | PRIOR APPLICATION NUMBER: 60/083554 |
| 59  | PRIOR APPLICATION NUMBER: 60/079786 | 60  | PRIOR FILING DATE: 1998-04-29       |
| 61  | PRIOR FILING DATE: 1998-03-27       | 62  | PRIOR APPLICATION NUMBER: 60/083558 |
| 63  | PRIOR APPLICATION NUMBER: 60/079920 | 64  | PRIOR FILING DATE: 1998-04-29       |
| 65  | PRIOR FILING DATE: 1998-03-30       | 66  | PRIOR APPLICATION NUMBER: 60/083559 |
| 67  | PRIOR APPLICATION NUMBER: 60/079923 | 68  | PRIOR FILING DATE: 1998-04-29       |
| 69  | PRIOR FILING DATE: 1998-03-30       | 70  | PRIOR APPLICATION NUMBER: 60/083500 |
| 71  | PRIOR APPLICATION NUMBER: 60/080105 | 72  | PRIOR FILING DATE: 1998-04-29       |
| 73  | PRIOR FILING DATE: 1998-03-31       | 74  | PRIOR APPLICATION NUMBER: 60/083742 |
| 75  | PRIOR APPLICATION NUMBER: 60/080107 | 76  | PRIOR FILING DATE: 1998-04-30       |
| 77  | PRIOR FILING DATE: 1998-03-31       | 78  | PRIOR APPLICATION NUMBER: 60/084366 |
| 79  | PRIOR APPLICATION NUMBER: 60/080165 | 80  | PRIOR FILING DATE: 1998-05-05       |
| 81  | PRIOR FILING DATE: 1998-03-31       | 82  | PRIOR APPLICATION NUMBER: 60/084414 |
| 83  | PRIOR APPLICATION NUMBER: 60/080194 | 84  | PRIOR FILING DATE: 1998-05-06       |
| 85  | PRIOR FILING DATE: 1998-03-31       | 86  | PRIOR APPLICATION NUMBER: 60/084441 |
| 87  | PRIOR APPLICATION NUMBER: 60/080327 | 88  | PRIOR FILING DATE: 1998-05-06       |
| 89  | PRIOR FILING DATE: 1998-04-01       | 90  | PRIOR APPLICATION NUMBER: 60/084637 |
| 91  | PRIOR APPLICATION NUMBER: 60/080328 | 92  | PRIOR FILING DATE: 1998-05-07       |
| 93  | PRIOR FILING DATE: 1998-04-01       | 94  | PRIOR APPLICATION NUMBER: 60/084639 |
| 95  | PRIOR APPLICATION NUMBER: 60/080333 | 96  | PRIOR FILING DATE: 1998-05-07       |
| 97  | PRIOR FILING DATE: 1998-04-01       | 98  | PRIOR APPLICATION NUMBER: 60/084640 |
| 99  | PRIOR APPLICATION NUMBER: 60/080334 | 100 | PRIOR FILING DATE: 1998-05-07       |
| 101 | PRIOR FILING DATE: 1998-04-01       | 102 | PRIOR APPLICATION NUMBER: 60/084598 |
| 103 | PRIOR APPLICATION NUMBER: 60/081070 | 104 | PRIOR FILING DATE: 1998-05-07       |
| 105 | PRIOR FILING DATE: 1998-04-08       | 106 | PRIOR APPLICATION NUMBER: 60/084600 |
| 107 | PRIOR APPLICATION NUMBER: 60/081049 | 108 | PRIOR FILING DATE: 1998-05-07       |
| 109 | PRIOR FILING DATE: 1998-04-08       | 110 | PRIOR APPLICATION NUMBER: 60/084627 |
| 111 | PRIOR APPLICATION NUMBER: 60/081071 | 112 | PRIOR FILING DATE: 1998-05-07       |
| 113 | PRIOR FILING DATE: 1998-04-08       | 114 | PRIOR APPLICATION NUMBER: 60/084643 |
| 115 | PRIOR APPLICATION NUMBER: 60/081195 | 116 | PRIOR FILING DATE: 1998-05-07       |
| 117 | PRIOR FILING DATE: 1998-04-08       | 118 | PRIOR APPLICATION NUMBER: 60/085339 |
| 119 | PRIOR APPLICATION NUMBER: 60/081203 | 120 | PRIOR FILING DATE: 1998-05-13       |
| 121 | PRIOR FILING DATE: 1998-04-09       | 122 | PRIOR APPLICATION NUMBER: 60/085338 |
| 123 | PRIOR APPLICATION NUMBER: 60/081229 | 124 | PRIOR FILING DATE: 1998-05-13       |
| 125 | PRIOR FILING DATE: 1998-04-09       | 126 | PRIOR APPLICATION NUMBER: 60/085323 |
| 127 | PRIOR APPLICATION NUMBER: 60/081955 | 128 | PRIOR FILING DATE: 1998-05-13       |
| 129 | PRIOR FILING DATE: 1998-04-15       | 130 | PRIOR APPLICATION NUMBER: 60/085582 |
| 131 | PRIOR APPLICATION NUMBER: 60/081817 | 132 | PRIOR FILING DATE: 1998-05-15       |
| 133 | PRIOR FILING DATE: 1998-04-15       | 134 | PRIOR APPLICATION NUMBER: 60/085700 |
| 135 | PRIOR APPLICATION NUMBER: 60/081819 | 136 | PRIOR FILING DATE: 1                |

;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.3e-225;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 1   | MGENDPFAVAPFSSRSLGLDLDLKISPVADADAVAQAQLLSLLPLKFFPIIVIGIIALI  | 60  |
| DB | 1   | MGENDPFAVAPFSSRSLGLDLDLKISPVADADAVAQAQLLSLLPLKFFPIIVIGIIALI  | 60  |
| QY | 61  | LALAIIGIHFDCSGKRYCRSSFKIELIARCDSVSDCKDGEDEYRCVRVGGQNAVLOVF   | 120 |
| DB | 61  | LALAIIGIHFDCSGKRYCRSSFKIELIARCDSVSDCKDGEDEYRCVRVGGQNAVLOVF   | 120 |
| QY | 121 | TAASWKTCSDWKGHYANVACAQLGFPSSVSSDNLVSSLEGGFEEFVSIDHLLPDDK     | 180 |
| DB | 121 | TAASWKTCSDWKGHYANVACAQLGFPSSVSSDNLVSSLEGGFEEFVSIDHLLPDDK     | 180 |
| QY | 181 | VTALHSHVYVREGCASGHVVTLOCTACGHRGYSRRIVGGMNLSLLSQWPQASLQFGYH   | 240 |
| DB | 181 | VTALHSHVYVREGCASGHVVTLOCTACGHRGYSRRIVGGMNLSLLSQWPQASLQFGYH   | 240 |
| QY | 241 | LCGGSVITPLWIIITAAHCVDYDLYLPKSWTIOGLVSLDNPAPSHLVEKIVYHSKYKPKR | 300 |
| DB | 241 | LCGGSVITPLWIIITAAHCVDYDLYLPKSWTIOGLVSLDNPAPSHLVEKIVYHSKYKPKR | 300 |
| QY | 301 | LGNDIALMKLAGLPTFNEMIQVCLPNSEENFPDCKVCTSGMGATEDGGDASPVNLHAA   | 360 |
| DB | 301 | LGNDIALMKLAGLPTFNEMIQVCLPNSEENFPDCKVCTSGMGATEDGGDASPVNLHAA   | 360 |
| QY | 361 | VPLISNICKNRDYGIIISPSMLCAGYLTGGVDSQCGSGGGLVCOERLWLKVGATSF     | 420 |
| DB | 361 | VPLISNICKNRDYGIIISPSMLCAGYLTGGVDSQCGSGGGLVCOERLWLKVGATSF     | 420 |
| QY | 421 | GIGCAEVNKPQGYTRVTSFLDWIHEQMERDLKT                            | 453 |
| DB | 421 | GIGCAEVNKPQGYTRVTSFLDWIHEQMERDLKT                            | 453 |

## RESULT 13

US-09-978-824-69  
Sequence 69, Application US/09978824  
Publication No. US20030055216A1  
GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavitz, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630P1C14  
;; CURRENT APPLICATION NUMBER: US/09/978,824  
;; CURRENT FILING DATE: 2001-10-17  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR FILING DATE: 1997-11-03  
;; PRIOR APPLICATION NUMBER: 60/065311  
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;; PRIOR APPLICATION NUMBER: 60/077450  
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;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080194  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080327  
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;; PRIOR APPLICATION NUMBER: 60/080328  
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;; PRIOR APPLICATION NUMBER: 60/080333  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080334  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/081070

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| 2  | PRIOR APPLICATION NUMBER: 60/081049 |
| 3  | PRIOR FILING DATE: 1998-04-08       |
| 4  | PRIOR APPLICATION NUMBER: 60/081071 |
| 5  | PRIOR FILING DATE: 1998-04-08       |
| 6  | PRIOR APPLICATION NUMBER: 60/081195 |
| 7  | PRIOR FILING DATE: 1998-04-08       |
| 8  | PRIOR APPLICATION NUMBER: 60/081203 |
| 9  | PRIOR FILING DATE: 1998-04-09       |
| 10 | PRIOR APPLICATION NUMBER: 60/081229 |
| 11 | PRIOR FILING DATE: 1998-04-09       |
| 12 | PRIOR APPLICATION NUMBER: 60/081955 |
| 13 | PRIOR FILING DATE: 1998-04-15       |
| 14 | PRIOR APPLICATION NUMBER: 60/081817 |
| 15 | PRIOR FILING DATE: 1998-04-15       |
| 16 | PRIOR APPLICATION NUMBER: 60/081819 |
| 17 | PRIOR FILING DATE: 1998-04-15       |
| 18 | PRIOR APPLICATION NUMBER: 60/081952 |
| 19 | PRIOR FILING DATE: 1998-04-15       |
| 20 | PRIOR APPLICATION NUMBER: 60/081838 |
| 21 | PRIOR FILING DATE: 1998-04-15       |
| 22 | PRIOR APPLICATION NUMBER: 60/082358 |
| 23 | PRIOR FILING DATE: 1998-04-21       |
| 24 | PRIOR APPLICATION NUMBER: 60/082569 |
| 25 | PRIOR FILING DATE: 1998-04-21       |
| 26 | PRIOR APPLICATION NUMBER: 60/082704 |
| 27 | PRIOR FILING DATE: 1998-04-22       |
| 28 | PRIOR APPLICATION NUMBER: 60/082804 |
| 29 | PRIOR FILING DATE: 1998-04-22       |
| 30 | PRIOR APPLICATION NUMBER: 60/082700 |
| 31 | PRIOR FILING DATE: 1998-04-22       |
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| 33 | PRIOR FILING DATE: 1998-04-22       |
| 34 | PRIOR APPLICATION NUMBER: 60/082796 |
| 35 | PRIOR FILING DATE: 1998-04-23       |
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| 38 | PRIOR APPLICATION NUMBER: 60/083322 |
| 39 | PRIOR FILING DATE: 1998-04-28       |
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| 42 | PRIOR APPLICATION NUMBER: 60/083495 |
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| 48 | PRIOR APPLICATION NUMBER: 60/083545 |
| 49 | PRIOR FILING DATE: 1998-04-29       |
| 50 | PRIOR APPLICATION NUMBER: 60/083554 |
| 51 | PRIOR FILING DATE: 1998-04-29       |
| 52 | PRIOR APPLICATION NUMBER: 60/083558 |
| 53 | PRIOR FILING DATE: 1998-04-29       |
| 54 | PRIOR APPLICATION NUMBER: 60/083559 |
| 55 | PRIOR FILING DATE: 1998-04-29       |
| 56 | PRIOR APPLICATION NUMBER: 60/083500 |
| 57 | PRIOR FILING DATE: 1998-04-29       |
| 58 | PRIOR APPLICATION NUMBER: 60/083742 |
| 59 | PRIOR FILING DATE: 1998-04-30       |
| 60 | PRIOR APPLICATION NUMBER: 60/084366 |
| 61 | PRIOR FILING DATE: 1998-05-05       |
| 62 | PRIOR APPLICATION NUMBER: 60/084414 |
| 63 | PRIOR FILING DATE: 1998-05-06       |
| 64 | PRIOR APPLICATION NUMBER: 60/084441 |
| 65 | PRIOR FILING DATE: 1998-05-06       |
| 66 | PRIOR APPLICATION NUMBER: 60/084537 |
| 67 | PRIOR FILING DATE: 1998-05-07       |
| 68 | PRIOR APPLICATION NUMBER: 60/084639 |
| 69 | PRIOR FILING DATE: 1998-05-07       |
| 70 | PRIOR APPLICATION NUMBER: 60/084640 |
| 71 | PRIOR FILING DATE: 1998-05-07       |
| 72 | PRIOR APPLICATION NUMBER: 60/084598 |
| 73 | PRIOR FILING DATE: 1998-05-07       |

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| 2  | PRIOR FILING DATE: 1998-5-07        |
| 3  | PRIOR APPLICATION NUMBER: 60/084627 |
| 4  | PRIOR FILING DATE: 1998-05-07       |
| 5  | PRIOR APPLICATION NUMBER: 60/084643 |
| 6  | PRIOR FILING DATE: 1998-05-07       |
| 7  | PRIOR APPLICATION NUMBER: 60/085339 |
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| 9  | PRIOR APPLICATION NUMBER: 60/085338 |
| 10 | PRIOR FILING DATE: 1998-05-13       |
| 11 | PRIOR APPLICATION NUMBER: 60/085323 |
| 12 | PRIOR FILING DATE: 1998-05-13       |
| 13 | PRIOR APPLICATION NUMBER: 60/085582 |
| 14 | PRIOR FILING DATE: 1998-05-15       |
| 15 | PRIOR APPLICATION NUMBER: 60/085700 |
| 16 | PRIOR FILING DATE: 1998-05-15       |
| 17 | PRIOR APPLICATION NUMBER: 60/085689 |
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| 21 | PRIOR APPLICATION NUMBER: 60/085580 |
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| 23 | PRIOR APPLICATION NUMBER: 60/085573 |
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| 27 | PRIOR APPLICATION NUMBER: 60/085697 |
| 28 | PRIOR FILING DATE: 1998-05-15       |

RESULT 14  
US-09-918-585A-69  
; Sequence 69, Application US/09918585A  
; Publication No. US2003060406A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHKEHAZI, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PICI  
CURRENT APPLICATION NUMBER: US/09/918,585A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/083559

;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083500  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084637  
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;; PRIOR APPLICATION NUMBER: 60/085700  
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;; PRIOR APPLICATION NUMBER: 60/085689  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 2443; DB 10; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.3e-225;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGENDPVAEPFRSLFGDLDDKISFVAPDADAVAAQILSLPLKFFPIIVIGIALI 60  
Db 1 MGENDPVAEPFRSLFGDLDDKISFVAPDADAVAAQILSLPLKFFPIIVIGIALI 60  
Qy 61 LALAIGLGHDFDCSGKRCRSSFKEIELIARCDGVSDCKDGEDEYRCVRYGGQNAVLOVF 120  
Db 61 LALAIGLGHDFDCSGKRCRSSFKEIELIARCDGVSDCKDGEDEYRCVRYGGQNAVLOVF 120  
Qy 121 TAASWKTCSDDWKGHYANVACQILGPFPSYSSDNLRVSSLEGQFREFVSIIDHLLPDDK 180  
Db 121 TAASWKTCSDDWKGHYANVACQILGPFPSYSSDNLRVSSLEGQFREFVSIIDHLLPDDK 180  
Qy 181 VTALHHSYVREGCASGHVVTLOCTACHRRRGYSRRVGGNMSLLSQWPQASLQFGYH 240  
Db 181 VTALHHSYVREGCASGHVVTLOCTACHRRRGYSRRVGGNMSLLSQWPQASLQFGYH 240  
Qy 241 LCGSVITPLMITAACHCYVDLYLPKSWTTQVGLVSLDDNPAPSHLVEKIVYHSKYKPKR 300  
Db 241 LCGSVITPLMITAACHCYVDLYLPKSWTTQVGLVSLDDNPAPSHLVEKIVYHSKYKPKR 300

Qy 301 LGNDIALMKLAGPLTFTNEMIQPVCLPNSSENFDDGKVCWTSGWGATEDGGDASPVLNHAA 360  
Db 301 LGNDIALMKLAGPLTFTNEMIQPVCLPNSSENFDDGKVCWTSGWGATEDGGDASPVLNHAA 360  
Qy 361 VPLISNKICNHRDVGIGIISPSMLCAGYLTGGVDSQCGSDGGPLVCQERRLKLVGATSF 420  
Db 361 VPLISNKICNHRDVGIGIISPSMLCAGYLTGGVDSQCGSDGGPLVCQERRLKLVGATSF 420  
Qy 421 GIGCAEVNKGVTYTRVTSFLDWIHEQWERDLKT 453  
Db 421 GIGCAEVNKGVTYTRVTSFLDWIHEQWERDLKT 453

RESULT 15

US-09-978-423A-69  
; Sequence 69, Application US/09978423A  
; Publication No. US20030069178A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C21  
; CURRENT APPLICATION NUMBER: US/09/978,423A  
; CURRENT FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
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; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR APPLICATION NUMBER: 60/077649  
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; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886

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3 PRIOR FILING DATE: 1998-03-20  
4 PRIOR APPLICATION NUMBER: 60/078910  
5 PRIOR FILING DATE: 1998-03-20  
6 PRIOR APPLICATION NUMBER: 60/078939  
7 PRIOR FILING DATE: 1998-03-20  
8 PRIOR APPLICATION NUMBER: 60/079294  
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73 PRIOR FILING DATE: 1998-04-22

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82 PRIOR APPLICATION NUMBER: 60/083392  
83 PRIOR FILING DATE: 1998-04-29  
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85 PRIOR FILING DATE: 1998-04-29  
86 PRIOR APPLICATION NUMBER: 60/083496  
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102 PRIOR APPLICATION NUMBER: 60/084366  
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104 PRIOR APPLICATION NUMBER: 60/084414  
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106 PRIOR APPLICATION NUMBER: 60/084441  
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109 PRIOR FILING DATE: 1998-05-07  
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111 PRIOR FILING DATE: 1998-05-07  
112 PRIOR APPLICATION NUMBER: 60/084640  
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129 PRIOR FILING DATE: 1998-05-15  
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135 PRIOR FILING DATE: 1998-05-15  
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139 PRIOR FILING DATE: 1998-05-15  
140 PRIOR APPLICATION NUMBER: 60/085704  
141 PRIOR FILING DATE: 1998-05-15  
142 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2,3e-225; Indels 0; Gaps 0;  
Matches 453; Conservative 0; Mismatches 0;

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| Qy | 1   | MGNDPPAVEAPFSPFSLFGLDDLKISPVAPDADAVAAQILSLPLKFPPIIVIGIIALI    | 60  |
| Db | 1   | MGNDPPAVEAPFSPFSLFGLDDLKISPVAPDADAVAAQILSLPLKFPPIIVIGIIALI    | 60  |
| Qy | 61  | LALAIGLGHFDCSGKYRCRSSPKCIJELJARCUGVSDCKDGRDEYRCVVGQNAVLOVF    | 120 |
| Db | 61  | LALAIGLGHFDCSGKYRCRSSPKCIJELJARCUGVSDCKDGRDEYRCVVGQNAVLOVF    | 120 |
| Qy | 121 | TAASWKTMCSDDDWKGHYANVACQAGFPSPVSSDNLRVSSLEGQFPREFVSIIDHLLPDDK | 180 |
| Db | 121 | TAASWKTMCSDDDWKGHYANVACQAGFPSPVSSDNLRVSSLEGQFPREFVSIIDHLLPDDK | 180 |
| Qy | 181 | VTALHHSVYVREGCASHVVTLOCTACGHRGYSRIVGNWSLLSOWPQASLOFQGYH       | 240 |
| Db | 181 | VTALHHSVYVREGCASHVVTLOCTACGHRGYSRIVGNWSLLSOWPQASLOFQGYH       | 240 |
| Qy | 241 | LCGGSVITPLWIIITAAHCYVDLYLPKSWTIQGLVSLDLNPNAPSHLVEKIVYHSKYKPKR | 300 |
| Db | 241 | LCGGSVITPLWIIITAAHCYVDLYLPKSWTIQGLVSLDLNPNAPSHLVEKIVYHSKYKPKR | 300 |
| Qy | 301 | LGNDIALMKLAGPLTNEMIQVCLPNSSENFDPGVKVCWTSGWGATEDGGDASPVLNHAA   | 360 |
| Db | 301 | LGNDIALMKLAGPLTNEMIQVCLPNSSENFDPGVKVCWTSGWGATEDGGDASPVLNHAA   | 360 |
| Qy | 361 | VPLISNKNHRDVGIIISPSMLCAGYLTGGVDSQGDSPGSLVCOERRLWKLVGATSF      | 420 |
| Db | 361 | VPLISNKNHRDVGIIISPSMLCAGYLTGGVDSQGDSPGSLVCOERRLWKLVGATSF      | 420 |
| Qy | 421 | GIGCAEVNKGVTYRTVTSFLDWIHEQWERDLKT                             | 453 |
| Db | 421 | GIGCAEVNKGVTYRTVTSFLDWIHEQWERDLKT                             | 453 |

Search completed: May 5, 2004, 15:54:14  
Job time : 49 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:44:50 ; Search time 20 Seconds  
(without alignments)  
2178.738 Million cell updates/sec

Title: US-09-846-512-2  
Perfect score: 2443  
Sequence: 1 MGENDPFAVEAPFERSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues 283366

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description            |
|------------|-------|-------------|--------|----------|------------------------|
| 1          | 674   | 27.6        | 417    | 1 S00845 | hepsin (EC 3.4.21.1)   |
| 2          | 669.5 | 27.4        | 1035   | 1 A43090 | enteropeptidase (E     |
| 3          | 664.5 | 27.2        | 1019   | 1 A56318 | enteropeptidase (E     |
| 4          | 663.5 | 27.2        | 1034   | 1 A53663 | enteropeptidase (E     |
| 5          | 654.5 | 26.8        | 416    | 1 S33777 | hepsin (EC 3.4.21.1)   |
| 6          | 579.5 | 23.7        | 638    | 1 KQRTPL | plasma kallikrein      |
| 7          | 570.5 | 23.4        | 638    | 1 KQMSPL | plasma kallikrein      |
| 8          | 553   | 22.6        | 855    | 2 JC7731 | membrane-bound arg     |
| 9          | 549.5 | 22.5        | 638    | 1 KQHUP  | plasma kallikrein      |
| 10         | 527   | 21.6        | 761    | 2 JC5759 | brain-specific ser     |
| 11         | 526   | 21.5        | 455    | 2 A61545 | plasmin (EC 3.4.21.1)  |
| 12         | 523.5 | 21.4        | 790    | 1 PLPG   | plasmin (EC 3.4.21.1)  |
| 13         | 506.5 | 20.7        | 1113   | 2 JF0315 | low-density lipopr     |
| 14         | 504   | 20.6        | 273    | 2 A47246 | tryptase (EC 3.4.21.1) |
| 15         | 504   | 20.6        | 625    | 1 KFHU1  | coagulation factor     |
| 16         | 504   | 20.6        | 812    | 1 PLMS   | plasmin (EC 3.4.21.1)  |
| 17         | 502   | 20.5        | 275    | 2 A32410 | tryptase (EC 3.4.21.1) |
| 18         | 502   | 20.5        | 810    | 1 PLHU   | plasmin (EC 3.4.21.1)  |
| 19         | 500.5 | 20.5        | 460    | 2 B61545 | plasmin (EC 3.4.21.1)  |
| 20         | 499   | 20.4        | 810    | 2 I46260 | plasmin (EC 3.4.21.1)  |
| 21         | 495.5 | 20.3        | 437    | 2 S18407 | acrosin (EC 3.4.21.1)  |
| 22         | 495   | 20.3        | 270    | 2 S56160 | mast cell tryptase     |
| 23         | 495   | 20.3        | 810    | 2 S30848 | plasmin (EC 3.4.21.1)  |
| 24         | 495   | 20.3        | 812    | 1 PLBO   | plasmin (EC 3.4.21.1)  |
| 25         | 493   | 20.2        | 276    | 2 A38654 | mast cell proteina     |
| 26         | 492   | 20.2        | 436    | 2 JX0172 | acrosin (EC 3.4.21.1)  |
| 27         | 492   | 20.1        | 418    | 2 A37344 | acrosin (EC 3.4.21.1)  |
| 28         | 490   | 20.1        | 274    | 2 J44171 | tryptase (EC 3.4.21.1) |
| 29         | 489   | 20.0        | 421    | 1 S11674 | acrosin (EC 3.4.21.1)  |

RESULT 1  
S00845  
hepsin (EC 3.4.21.-) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999  
C:Accession: S00845  
R:Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.  
Biochemistry 27, 1067-1074, 1988  
A:Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain  
A:Reference number: S00845; MUID:88209431; PMID:2835076  
A:Accession: S00845  
A:Molecule type: mRNA  
A:Residues: 1-417 <LEY>  
A:Cross-references: ENBL:X07732; NID:G32063; PIDN:CAA30558.1; PID:G32064  
C:Genetics:  
A:Gene: GDB:HPN; TMRSS1; hepsin  
A:Cross-references: GDB:135685; OMIM:142440  
A:Map position: 19q11-19q13.2  
C:Superfamily: hepsin; trypsin homology  
C:Keywords: hydrolase; liver; serine proteinase; transmembrane protein  
F:23-45/Domain: transmembrane #status predicted <TMN>  
F:163-400/Domain: trypsin homology <TRY>  
F:188-204, 291-359, 322-338, 349-381/Disulfide bonds: #status predicted  
F:203, 257, 353/Active site: His, Asp, Ser #status predicted

ALIGNMENTS

|    |       |      |      |   |        |                            |
|----|-------|------|------|---|--------|----------------------------|
| 30 | 488   | 20.0 | 431  | 2 | S47538 | acrosin (EC 3.4.21.1)      |
| 31 | 482   | 19.7 | 275  | 2 | A35863 | tryptase (EC 3.4.21.1)     |
| 32 | 481   | 19.7 | 275  | 2 | B35863 | tryptase (EC 3.4.21.1)     |
| 33 | 478   | 19.6 | 343  | 1 | A57014 | proctasin (EC 3.4.21.1)    |
| 34 | 476.5 | 19.5 | 264  | 2 | I38136 | chymotrypsin-like          |
| 35 | 476   | 19.5 | 275  | 2 | C35863 | tryptase (EC 3.4.21.1)     |
| 36 | 472   | 19.3 | 421  | 2 | S29599 | acrosin (EC 3.4.21.1)      |
| 37 | 469.5 | 19.2 | 1524 | 2 | T30337 | polyprotein - Afri1        |
| 38 | 467   | 19.1 | 263  | 1 | KVETB  | chymotrypsin (EC 3.4.21.1) |
| 39 | 466   | 19.1 | 263  | 2 | A31239 | chymotrypsin (EC 3.4.21.1) |
| 40 | 465   | 19.0 | 263  | 2 | A21195 | tryptase (EC 3.4.21.1)     |
| 41 | 464.5 | 19.0 | 274  | 2 | A45754 | trypsin (EC 3.4.21.1)      |
| 42 | 463   | 19.0 | 277  | 2 | S35340 | acrosin (EC 3.4.21.1)      |
| 43 | 463   | 19.0 | 415  | 1 | A34170 | chymotrypsin (EC 3.4.21.1) |
| 44 | 462   | 18.9 | 263  | 2 | S47537 | chymotrypsin (EC 3.4.21.1) |
| 45 | 461   | 18.9 | 275  | 2 | S40005 | trypsin (EC 3.4.21.1)      |

|    |     |   |     |                           |   |
|----|-----|---|-----|---------------------------|---|
| QY | 59  | LTLALAIGLIHFDGCGKYRCRSPKCELIARCDGVSDCKDGEYRCVVGQNAVLQ       | 118 | Query Match               | 27.6%; Score 674; DB 1; Length 417;     |
| Db | 26  | LLLLTAIG-----AASWAIYAVILRED-----QEPLYPQVSSADARLM            | 64  | Best Local Similarity     | 35.8%; Pred. No. 1.7e-46;               |
| QY | 119 | VF--TAASWKMCDDWKGHYANVACAQGLFPFVYSSNLRVSSLEGGFREFVSDHLL     | 176 | Matches 149; Conservative | 62; Mismatches 143; Indels 62; Gaps 11; |
| Db | 65  | VFDKTEGTWLLCCSSRNARVAGLSCEMGFLRALTHSELDVRTAGANGTSFGFCVDB--  | 122 |                           |   |
| QY | 177 | PDDKVTALHHSVYVE-----GCASGHVVTIQTACGHRGYSRRVGGNMSLLSQWPWQ    | 231 |                           |   |
| Db | 123 | -----GRPHYORLLEVISVDCDPRGFLAICQDCGRKLPVDRIVGGRTSLGRWPWQ     | 177 |                           |   |
| QY | 232 | ASLQFGVHLCGGSVITPLWITAAHCVYDLYLPK-----SWTQVGLVLLNPAFSPH     | 285 |                           |   |
| Db | 178 | VSLRYDGAHLCCGSLSGDWLVLTAAHC-----FPERNEVLNRVRFAGAVA---QASPHG | 229 |                           |   |
| QY | 286 | L---VEKIVYHSHYKPKR-----LGNDAIMKLAGPLTFNEMIOVCLPNSSENFPGK    | 336 |                           |   |
| Db | 230 | LQIGVQVAVYHGGYLPFFRDPNSENNDIALVHLLSPPLTEYIIOFVLPRAGQALVGGK  | 289 |                           |   |
| QY | 337 | VCWTSWGATGCGDASPVINHAAPLISNKICNHRDVIYGGIISPSMFCAGYLTGQVDS   | 396 |                           |   |
| Db | 290 | ICTVTGNGNTQYGGQAGVLOEARVPIISNDVNCADFYGNQIKPKMFCAGYPEGGIDAC  | 349 |                           |   |

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QY 397 QGDSGPLYCOE-----RRLLKLVGATSGFGICAEVNVKPGVYTVTSFLDWIHEOME 448
DB 350 QGDSGPFVCEDSISKTPRWLCGIVSWGTCALAKPGVYTKVSDFRWIFQAIK 405

RESULT 2
A43090
enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine
N/Alternate names: enterokinase
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Apr-2003
C/Accession: A43090; A48874; A61436
R/Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A/Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of two distinct domains
A/Reference number: A43090, MUID:94329561, PMID:8952624
A/Accession: A43090
A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1035 <KIT>
A/Cross-references: GB:U09859; NID:G746410; PIDN:AAB40026.1; PID:G746411
R/LaValle, E.R.; Rehmetulla, A.; Racie, L.A.; DiBiasio, E.A.; Ferez, C.; Grant, K.L.; J. Biol. Chem. 268, 23311-23317, 1993
A/Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of bovine enterokinase
A/Reference number: A48874, MUID:94043122; PMID:8226855
A/Accession: A48874
A/Molecule type: mRNA
A/Residues: 801-1035 <LAV>
A/Cross-references: GB:L19663; NID:G416131; PIDN:AAA16035.1; PID:G416132
A/Note: parts of this sequence, including the amino end of the mature protein, were confirmed by N-terminal sequencing
R/Light, A.; Janska, H. J. Protein Chem. 10, 475-480, 1991
A/Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase
A/Reference number: A61436; MUID:92189715; PMID:1799406
A/Accession: A61436
A/Molecule type: protein
A/Residues: 801-807, 'Y', 809-827 <LIG>
C/Comment: The mechanism of association with the membrane of the intestinal brush border enzyme attachment using a signal-anchor sequence.
C/Comment: Conversion from membrane-bound to soluble forms may involve further processing
C/Complex: mature enteropeptidase is variously reported to contain two (heavy and light) lide linked
C/Function:
A/Description: cleaves propeptide from trypsinogen to produce active trypsin
A/Pathway: intestinal digestive hydrolase cascade
C/Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat homology
C/Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein
F/22-38/Domain: transmembrane #status predicted <TM>
F/52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F/118-800/Product: enteropeptidase heavy chain #status predicted <HCH>
F/199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/338-520/Domain: MAM homology <MAM>
F/542-647/Domain: C1r/C1s repeat homology <C1R>
F/659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/694-799/Domain: scavenger receptor cysteine-rich domain homology #status predicted <LCH>
F/801-1035/Domain: enteropeptidase light chain #status predicted <LCH>
F/801-1035/Domain: trypsin homology <TRY>
F/116-147, 179, 328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site: His, Asp, Ser #status predicted
F/788-922, 826-842, 926-993, 957-972, 983-1011/Disulfide bonds: #status predicted
F/841, 892, 987/Active site: His, Asp, Ser #status predicted

Query Match 27.4%; Score 669.5; DB 1; Length 1035;
Best Local Similarity 37.0%; Pred. No. 1.2e-45;
Matches 146; Conservative 70; Mismatches 146; Indels 33; Gaps 14;

QY 66 GLGHFDC-SKGYCRSFKIELIARCDGVSCCKGDEYRCVRV---GGQNAVLYQVF 120
DB 652 GLGPEPKEDNFCKDG-ECIPLVNLCDGFFHCKGSDGAHCVRFLNFTGTTSSGLVQFR 710
QY 121 TAASWTKMCSDDWKGHYANVACALGPFPSVSSNLRVSSLEQGQFRFEFVSIDHLLPDDK 180

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DB 711 IQSIHWACAEENWTTQISDDVCQLLIGT--GNSSVPTFTSGG---GPVYNLN----- 758
QY 181 VTALHHSVYV--REGCASGHVVTLOCT--ACGHR---RGVSSRIVGNNMSSLISOWPQOAS 233
DB 759 -TAENGSLIITPQOCCLEDSLIILQCNYSKCGKLVTOEVPSPKIVGSGSREGAMPNVVA 817
QY 234 LQFGYHLGCGSVITPLWIIITAAHCVVYDYL-PKSWTIQVGL--VSLDNP-APSHLVEK 289
DB 818 LYPDDQVCGASLVSRLVLSAAHCVVGRNVNPEKSKAVLGLEWASNLTSFQIETRLIDQ 877
QY 290 IVYHSKYKPKRLGNIDIALMKLAGPLTFNEMIQVCLPNSSENPDPGKVCWTSQWGATEDG 349
DB 878 IVINPHYKRRKKNNDIAMHLEMKVNTDIQICLPEENQVFPFGRICSIAGWGALIYQ 937
QY 350 GDASFVNLNAAVPLISNKNR-DVYGGIISPSMILCAGYLTGCGVDSQCGSDSGGPLVCOE 408
DB 938 GSTADVLQEAQVPLLSNEKQCOQMPYN--ITENMVCAVEAGGVDSQCGSDSGGPLMCOE 995
QY 409 RRLKLVGATSGFGICAEVNVKPGVYTVTSFLDWI 443
DB 996 NNRLLAGVTSFGYQCALPNRPGVYARVPRFTEMI 1030

RESULT 3
A56318
enteropeptidase (EC 3.4.21.9) precursor [validated] - human
N/Alternate names: enterokinase
C/Species: Homo sapiens (man)
C/Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
C/Accession: A56318; B43090
R/Kitamoto, Y.; Veille, R.A.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A/Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic initiator of intestinal digestion
A/Reference number: A56318; MUID:95234679; PMID:7718557
A/Accession: A56318
A/Molecule type: mRNA
A/Residues: 1-1019 <KIT>
A/Cross-references: GB:U09860; NID:G746412; PIDN:AAC50138.1; PID:G746413
R/Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A/Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of two distinct domains
A/Reference number: A43090; MUID:94329561; PMID:8952624
A/Accession: B43090
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 749-1019 <KI2>
A/Cross-references: GB:U09860
C/Comment: The mechanism of association with the membrane of the intestinal brush border enzyme attachment using a signal-anchor sequence.
C/Complex: mature enteropeptidase is variously reported to contain two (heavy and light) lide linked
C/Function:
A/Description: cleaves activation peptide from trypsinogen to produce active trypsin
A/Pathway: intestinal digestive hydrolase cascade
C/Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat homology
C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F/1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
F/22-38/Domain: transmembrane #status predicted <TM>
F/184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/526-631/Domain: C1r/C1s repeat homology <C1R>
F/643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/678-783/Domain: scavenger receptor cysteine-rich domain homology #status predicted <LCH>
F/785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F/116, 147, 179, 328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site: His, Asp, Ser #status predicted
F/772-896, 810-826, 910-977, 941-956, 967-995/Disulfide bonds: #status predicted
F/825, 876, 971/Active site: His, Asp, Ser #status predicted

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Query Match 27.2%; Score 664.5; DB 1; Length 1019;  
Best Local Similarity 37.5%; Pred. No. 2.9e-45;  
Matches 147; Conservative 67; Mismatches 149; Indels 29; Gaps 14;

QY 67 LGHFDC-SGKYRCRSFKCIELIARCDGVSCKDGEDEYRCV- - - VGGQNAVLOVFT 121  
DB 637 LGIPECKADHFOCKNG-ECVPLVNI-CDGHLCEGDSDEADCVRFNGTNNGLVRPI 695  
QY 122 AASWTKMCSDDWKGHYANVACAOQGFPSYVSSDNLVSSLEQGFREBFVSIIDHLLPDDKV 181  
DB 696 QSIWHTACAEWNTTQISNDVQCQLLGGSGNSSK- -PIFSTDG- - -GPVFKL-NTAPDG- - 747  
QY 182 TALHHSVYVREGCASGHVVTLOCT- -ACGHR- - -RGYSSRIIVGGNMSLLSQWPMQASLOP 236  
DB 748 - - -HLILTSQQLQDLSRLQCNHKSCKKAAQDITPKIVGGNAKGGAPWVVGLYI 804  
QY 237 QGYHLCGGSVITPLMIITAAHCYVDLYL- -PKSWTIQVGL- - -VSLLDNP-APSHLVEKI 292  
DB 805 GGRLLCGASLVSSDMLVSAHCVYGRNLFPSPKWTALGLHMKSNLTSPQTVPRLLIDEIVI 864  
QY 293 HSKYKPKRLGNDIALMKLAGPLTFNEMIQVCLPNSSENFDPGKVCWTSWGATEDGG 352  
DB 865 NPHYNNRRKNDIAMHLEFKVNYTDYIQICLPENQVFPFGNRCIAGWGTVYVQGT 924  
QY 353 SPVLNHAAPVLIISNKICNHR- -DVYGGIISPSMLCAGYLTGGVDSQCGSGGGLVQCOERL 411  
DB 925 ANILQEADVPLLSNERCQQQMPYNN- -ITENMICAGYEBGGIDSCQDGGSGGLMCOENR 982  
QY 412 WKLVGATSGIGCAEVNKPFGVYTRVTSFLDWI 443  
DB 983 WFLAGVTSFGYKCALPNRPGVYARVPRKTEWI 1014

RESULT 4  
A53663  
enteropeptidase (EC 3.4.21.9) precursor [validated] - pig  
N/Alternate names: enterokinase  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 07-Oct-1994 #sequence\_revision 09-Aug-1996 #text\_change 28-Apr-2003  
C/Accession: A53663  
R/Matsushima, M.; Ichinose, M.; Vahagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa, J. Biol. Chem. 269, 19976-19982, 1994  
A/Title: Structural characterization of porcine enteropeptidase.  
A/Comment: The mechanism of association with the membrane of the intestinal brush border (ated below) or with amino-terminal myristoylation of the heavy chain.  
A/Complex: Mature enteropeptidase is variously reported to contain two (heavy and light) ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv  
C/Function:  
A/Description: cleaves activation peptide from trypsinogen to produce active trypsin  
A/Pathway: intestinal digestive hydrolase cascade  
C/Superfamily: enteropeptidase; Clr/Cis repeat homology; LDL receptor ligand-binding rep  
F/22-38/Domain: transmembrane #status predicted <TM>  
F/52-117/Product: enteropeptidase mini chain #status predicted <MCH>  
F/118-799/Product: enteropeptidase heavy chain #status predicted <HCH>  
F/199-236/Domain: LDL receptor ligand-binding repeat homology <LDL>  
F/237-319/Domain: MAM homology <MAM>  
F/341-646/Domain: Clr/Cis repeat homology <Clr>  
F/658-798/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F/800-1034/Product: scavenger receptor cysteine-rich domain homology #status atypical <SRC>  
F/800-1029/Domain: enteropeptidase light chain #status predicted <LCH>  
F/116-147, 170, 194, 283, 343, 350, 403, 455, 485, 518, 549, 645, 697, 701, 721, 740, 761, 804, 863, 902, 96  
F/787-911, 825-841, 925-992, 956-971, 982-1010/Disulfide bonds: #status predicted  
F/840, 891, 986/Active site: His, Asp, Ser #status predicted

Query Match 27.2%; Score 663.5; DB 1; Length 1034;  
Best Local Similarity 37.8%; Pred. No. 3.5e-45;  
Matches 149; Conservative 65; Mismatches 147; Indels 33; Gaps 14;

QY 67 LGHFDC-SGKYRCRSFKCIELIARCDGVSCKDGEDEYRCV- - - VGGQNAVLOVFT 121  
DB 652 LGIPECKEDNFOCKNG-ECVLLVNLCDGFSCKDGSDEAHCVRFNLGTANNGLVQFRI 710  
QY 122 AASWTKMCSDDWKGHYANVACAOQGFPSYVSSDNLVSSLEQGFREBFVSIIDHLLPDDKV 181  
DB 711 QSIWHTACAEWNTTQISDDVQCQLLGGTGNSSMPF- -FSSGGG- - -PFVKLN- - - 757  
QY 182 TALHHSVYV- - -REGCASGHVVTLOCT- -ACGHR- - -RGYSSRIIVGGNMSLLSQWPMQASL 234  
DB 758 TAPNGSLILITASEQCFEDSLILQCNHKSCKKQVAGVSPKIVGGNDSREGAPWVVAL 817  
QY 235 QGYHLCGGSVITPLMIITAAHCYVDLYL- -PKSWTIQVGL- - -VSLLDNP-APSHLVEKI 290  
DB 818 YNGQLLCGASLVSSDMLVSAHCVYGRNLFPSPKWTALGLHMKSNLTSPQIVTRLLIDEI 877  
QY 291 VYHSKYKPKRLGNDIALMKLAGPLTFNEMIQVCLPNSSENFDPGKVCWTSWGATEDGG 350  
DB 878 VINPHYNNRRKNDIAMHLEFKVNYTDYIQICLPENQVFPFGNRCIAGWGTVYVQGT 937  
QY 351 DASPVNHAAPVLIISNKICNHR- -DVYGGIISPSMLCAGYLTGGVDSQCGSGGGLVQCOER 409  
DB 938 SPADILQEADVPLLSNERCQQQMPYNN- -ITENMICAGYEBGGIDSCQDGGSGGLMCOEN 995  
QY 410 RLKLVGATSGIGCAEVNKPFGVYTRVTSFLDWI 443  
DB 996 NRLLAGVTSFGYKCALPNRPGVYARVPRKTEWI 1029

RESULT 5  
S33777  
hepsin (EC 3.4.21.-) - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 18-Jun-1999  
C/Accession: S33777; S32013  
R/Farley, D.; Raymond, F.; Nick, H. Biochim. Biophys. Acta 1173, 350-352, 1993  
A/Title: Cloning and sequence analysis of rat hepsin, a cell surface serine proteinase.  
A/Reference number: S33777; MUID:93305733; PMID:8318546  
A/Accession: S33777  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-416 <FAR>  
A/Cross-references: ENBL:X70900; NID:957928; PIDN:CAA50256.1; PID:957929  
C/Superfamily: hepsin; trypsin homology  
C/Keywords: hydrolase; liver; serine proteinase; transmembrane protein  
F/22-44/Domain: transmembrane #status predicted <TM>  
F/162-399/Product: trypsin homology <tr>  
F/187-203, 290-358, 321-337, 348-380/Disulfide bonds: #status predicted  
F/202, 256, 352/Active site: His, Asp, Ser #status predicted

Query Match 26.8%; Score 654.5; DB 1; Length 416;  
Best Local Similarity 35.3%; Pred. No. 6.4e-45;  
Matches 146; Conservative 61; Mismatches 156; Indels 51; Gaps 10;

QY 60 ILAIAIGLGHFDGSGKYRCRSFKCIELIARCDGVSCKDGEDEYRCVGGQNAVLOV 119  
DB 17 VAALTGTGTLLELTGIG- - -AASWAIIVTILR- - -SDQEPLYQVQLSPGDSRLVL 65  
QY 120 -FTAASWTKMCSDDWKGHYANVACAOQGFPSYVSSDNLVSSLEQGFREBFVSIID- - - 173  
DB 66 DKTEGTWELLCSSRSNARVAGLGEEMGFLRALHSELDTVITAGANGTSFFCVDEGLP 125  
QY 174 - - -HLLPDDKVYTAALHSHSVYVREGCASGHVVTLOCTACGHRGYSRIVGGNMSLLSQWPM 230  
DB 126 LAQRL- - -DVISVC- - - -DCPRGRFLITATCQDGRRLPVDRIVGGDSSGLGRPW 175  
QY 231 QASLQFGYHLCGGSVITPLMIITAAHCYVDLYL- - -SWTIQVGLVSLLDNPAPS 284

Db 176 QVSLRYDGLHLCGSLSGDWLTAHC-----FPERNRVLSRWVAFAGAVARTSPHAVQ 230  
 QY 285 HLVEKIVYHSKYKPKR-----LGNDIALMKLAGPLTFTNEMIQVCLPNSSENFDPDGKVC 338  
 Db 231 LGVQAVIYHGGYLPFRDPTIDNSNDIALVHLSSSLPLTEYIQVCLPAAGQALVDGKVC 290  
 QY 339 WTSWGATGEGDGDAPVNLHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSQCG 398  
 Db 291 TVTGWNTQFYQQAVVLQEARVPLISNEVCNPSDFYGNQIKPKWFCAGYPEGGLDACQG 350  
 QY 399 DSGGGLVLCQER----RLMKLVGATSGIGCAEVNRPFGVYTRVTSFLDWIHSQME 448  
 Db 351 DSGGHFVCDRIISGTSRWLGVISWGTGCLARKPGVVYTKVIDFREMIFQAIA 404  
 RESULT 6  
 KQRIPL  
 plasma kallikrein (EC 3.4.21.34) precursor - rat  
 N:Alternate names: Fletcher factor; kininogenin; serum kallikrein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999  
 C:Accession: A3180; A3320; S06851; I53041; S06852  
 R:Seaidah, N.G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.; Seidah, N.G.  
 Biochemistry 30, 1628-1635, 1991  
 A:Title: Gene structure and chromosomal localization of plasma kallikrein.  
 A:Reference number: A39180; MUID:91129236; PMID:1993180  
 A:Accession: A39180  
 A:Molecule type: DNA  
 A:Residues: 1-638 <BEA>  
 A:Cross-references: GB:J03315  
 A:Note: the authors translated the codon GAG for residue 81 as Gln  
 R:Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, F.; Lazur  
 DNA 8, 563-574, 1989  
 A:Title: The cDNA structure of rat plasma kallikrein.  
 A:Reference number: A33320; MUID:90091743; PMID:2598771  
 A:Accession: A33320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <SEI>  
 A:Cross-references: GB:M30282; NID:G205010; PIDN:AAA41463.1; PID:G205011  
 A:Note: part of this sequence, including the amino ends of both the heavy and light chain  
 R:Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, N.G.  
 Biochim. Biophys. Acta 999, 103-110, 1989  
 A:Title: Rat plasma kallikrein: purification, NH(2)-terminal sequencing and development  
 A:Reference number: S06851; MUID:90089457; PMID:2597701  
 A:Accession: S06851  
 A:Molecule type: protein  
 A:Residues: 20-45; 391-413 <PAQ>  
 R:Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, F.; Lazur  
 DNA Cell Biol. 8, 563-574, 1989  
 A:Title: The cDNA structure of rat plasma kallikrein.  
 A:Reference number: I53041  
 A:Accession: I53041  
 A>Status: translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <RES>  
 A:Cross-references: GB:M58590; NID:G206721; PIDN:AAA42069.1; PID:G206722  
 A:Note: This protein, synthesized in the liver, circulates as a noncovalent complex w  
 C:Comment: The zymogen is activated by factor XIII, which cleaves the molecule into a li  
 are linked by one or more disulfide bonds.  
 C:Genetics:  
 A:Gene: PK  
 C:Superfamily: coagulation factor XI; trypsin homology  
 C:Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-390/Product: plasma kallikrein heavy chain #status experimental <MAT1>  
 F:20-109/Domain: apple repeat <AP1>  
 F:110-199/Domain: apple repeat <AP2>  
 F:200-289/Domain: apple repeat <AP3>  
 F:291-380/Domain: apple repeat <AP4>  
 F:391-638/Product: plasma kallikrein light chain #status experimental <MAT2>  
 F:391-621/Domain: trypsin homology <TRY>  
 F:21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322

F:127,215,308,453,459,494/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:396/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:434,483,578/Active site: His, Asp, Ser #status predicted  
 Query Match 23.7%; Score 579.5; DB 1; Length 638;  
 Best Local Similarity 41.0%; Pred. No. 1.1e-38;  
 Matches 116; Conservative 52; Mismatches 88; Indels 27; Gaps 8;  
 QY 189 YVREGCASGHVTL-----QCTACGHRGVSRRVGGNMSSLLSQWPMQASIQFQ---G 238  
 Db 362 YEAGQ-SSGYSRLCKVWESSDCTT-----KINARIVGGTNSLGEWPMQVSLQVKLSQ 415  
 QY 239 YHLCGGSVITPLWIIITAAHCYVDLYLPSKSWTTQVGLVSL--LDNFAPSHLVKIVVHSKY 296  
 Db 416 NEMCGSIIIGRWILTAHCFDGIPIYDVRVGVGILNLSEITNKTFFSSIKELIHHQKY 475  
 QY 297 KPKRLGNDIALMKLAGPLTFNEMIQVCLPNSSENFDPDGKVCWTSWGATGEGDGDAPV 356  
 Db 476 KMSGSGYDIALIKLQPLNTEYFQKPCICLSKADNTIYTNVTCWVTGWTKRGERTQNIL 535  
 QY 357 NHAAPVLSNKIC--NHRDVYGGIISPSMLCAGYLTGGVDSQCGSGGLVLCQERLWL 414  
 Db 536 QKATIPLVFNEECQKYRDI--VITKQMLCAGYKEGGIDACKGDSGGLVCKHSGRWQL 592  
 QY 415 VGTSTFGIGCAEVNRPFGVYTRVTSFLDWIHSQME----ERDLKT 453  
 Db 593 VGITSWGEGCARKEQPGVYTKVAEYIDWILEKIQSSKERALET 635  
 RESULT 7  
 KQMSPL  
 plasma kallikrein (EC 3.4.21.34) precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999  
 C:Accession: A36557  
 R:Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont  
 DNA Cell Biol. 9, 737-748, 1990  
 A:Title: Mouse plasma kallikrein: cDNA structure, enzyme characterization, and comparison  
 A:Reference number: A36557; MUID:91090844; PMID:2264928  
 A:Accession: A36557  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <SEI>  
 A:Cross-references: GB:M58588; NID:G200358; PIDN:AAA63393.1; PID:G200359  
 A:Note: part of this sequence, including the amino ends of both the heavy and light chain  
 C:Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w  
 are linked by one or more disulfide bonds.  
 C:Superfamily: coagulation factor XI; trypsin homology  
 C:Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-390/Product: plasma kallikrein heavy chain #status experimental <HCH>  
 F:20-109/Domain: apple repeat <AP1>  
 F:110-199/Domain: apple repeat <AP2>  
 F:200-289/Domain: apple repeat <AP3>  
 F:291-380/Domain: apple repeat <AP4>  
 F:391-638/Product: plasma kallikrein light chain #status experimental <LCH>  
 F:391-621/Domain: trypsin homology <TRY>  
 F:21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-  
 F:127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:434,483,578/Active site: His, Asp, Ser #status predicted  
 Query Match 23.4%; Score 570.5; DB 1; Length 638;  
 Best Local Similarity 34.9%; Pred. No. 6e-38;  
 Matches 126; Conservative 61; Mismatches 109; Indels 65; Gaps 11;  
 QY 132 DWKGHYANVACAQIGFSPYSSDNLRYSSLEGQFEEFVSDHLLPDKVTALHHSVYVR 191  
 Db 301 DFEGEELNV-----TFVQAGDVCOETCTKTIRCOFF-IYSLPDD-----CKE 342  
 QY 192 EGC-----ASGHVVTL-----QCTACGHRGVSRRVGGNMSSLLSQWPMQASIQFQ---G 238  
 Db 343 EGCKSLRLSDGSPTRITYGMQSSGSLRLCKLVDSPDCTT-----KINARIVGGTNA 397

267 ---SWTIOGVGLVLLDNPA---PSHLVEKIVTHYSKYPKRLGNDIALMKLAGPLTENEI 320  
668 DHTWTAFLGLLDOSKKSASGVQEHKUKRIITHPSFNDFDYDIALLELEKPAEYSTVV 727  
321 QPVCPLNSENFDPGKYCVCTSGWGATGGDAGFVLNHAAPLISNKICNHRDPVYGIIIS 380  
728 RPICLPDNTHVFPAGKAIWTVGWGTEKGGTGALILQKGEIRVINQTTCC--BELLPQQIIT 785  
381 PSMLCAGYLTCGVDS CGDGGGGLVCOER--RLWLKVLGATSFSGIGAEVNVKPGVYTRVTS 438  
786 PRMVCVGLSGVDSCQDGGSGGLPSSVEKQGRIFQ-AGVSVWEGGCAQNRKPGVYTRIPE 844  
439 FLDWIHEQ 446  
845 VRDWIKQ 852

QY DB

RESULT 9  
KOHUP  
Plasma kallikrein (EC 3.4.21.34) precursor - human  
A:Alternate names: kiningenin; plasma prekallikrein  
C:Species: Homo sapiens (man)  
C:Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 18-Jun-1999  
C:Accession: A00921; A37939  
R:Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.  
Biochemistry 25, 2410-2417, 1986  
A:Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four t.  
A:Reference number: A00921; PMID:86243359; PMID:3521732  
A:Accession: A00921  
A:Molecule type: mRNA  
A:Residues: 1-638 <CHU>  
A:Cross-references: GB:MI3143; NID:G190262; PIDN:AAA60153.1; PID:G190263  
R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.  
Biochemistry 30, 2050-2056, 1991  
A:Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of  
A:Reference number: A37939; PMID:91152016; PMID:1958666  
A:Accession: A37939  
A:Molecule type: protein  
A:Residues: 20-27;40-46,'X',48,'H',50,'X',52-70,'H',75-76,'X',78-80;103-113;131-140;141-  
1560-283,'X',285;287-291,'X',293-295;314-317,'X',319-320;321-324,'X',329-333;334-339,'X',  
525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 <MCM>  
C:Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w  
C:Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a li  
are linked by one or more disulfide bonds.  
C:Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal r  
ingen and may also play a role in the renin-angiotensin system by converting prorenin in  
C:Genetics:  
A:Gene: GDB:KLK3  
A:Cross-references: GDB:127575; OMIM:229000  
A:Map position: 4q35-q35  
C:Superfamily: coagulation factor XI; trypsin homology  
C:Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-638/Product: plasma kallikrein #status predicted <MAT>  
F:20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>  
F:20-109/Domain: apple repeat <AP1>  
F:110-199/Domain: apple repeat <AP2>  
F:200-289/Domain: apple repeat <AP3>  
F:291-380/Domain: apple repeat <AP4>  
F:391-638/Domain: plasma kallikrein light chain #status predicted <LCH>  
F:391-621/Domain: trypsin homology <TRY>  
F:21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383  
F:127,308,396,433,494/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:318-347,340-345/disulfide bonds: #status predicted (Asn) (covalent) #status experimental  
F:390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted  
F:434,483,578/Active site: His, Asp, Ser #status predicted

Query Watch 22.5%; Score 549.5; DB 1; Length 638;  
Best Local Similarity 35.8%; Pred No. 2,9e-36;  
Matches 124; Conservative 57; Mismatches 116; Indels 49; Gaps 11;

QY 132 DWKGHYANVACQLOQPPSYVSDNLRVSLSGQFEEFVSDIHLPLDD----- 179

301 DFGGELNV-----TFVGNVNCQETCTKMKRCQFFTVS--LLPEDCCKSEKCKFURL 351  
180 ----KVTALHHSVYREGCASGRVVTL-----DCTACGHRGYSRRIVGNNMLLSQW 228  
352 SMDGSPTRI---AYGTQG--SGYSRLCNTGNSVCTT-----KSTRIVGNTSSWGEM 402  
229 PQASLQFO---GYHLCGSGVITPWIITAAHCVDLYLPKSWTTIQGLVSLLD--NPAP 283  
403 PMQVSLQVLTAQRHLCCGSLTGHQVWLVAAHCFDGLPLQDVWRIYSGILNLSLDTKOTP 462  
284 SHLVEKIVYHSKYKPKRLGNDIALMKLAGLPTFNEMIQVCLPNSGEENFPDQKVCWTSGW 343  
463 FSGIKELIHHQYKVSSEGNHDLALIKLQAPLVNTEFQKPICLPSKGDSTIYTNQWVTGW 522  
344 GATEDGGDASPVLNHAAVPLNISKNICNHRDVTGGI--ISPSMLCAGYLIGVDSCQDGG 402  
523 GFSKERGEIQNIIQKVINPLVTEECQKR--YQDYKITQRMVCAGYKEGGKADCKDGG 580  
403 PLVQERRRLKLGATSGFSGCAEVNKPVGVTYRTVTSFLDWIHEQME 448  
581 PLVCKRNGMRLVGIISWEGGCARRQPGVGYTKVAEYMDVILEKTQ 626

RESULT 10  
JC5759  
A:Species: Mus musculus (house mouse)  
C:Date: 24-Jan-1998 #sequence\_revision 13-Mar-1998 #text\_change 31-Mar-2000  
R:Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.; Tsumimura, A.; Yamaguchi, N.  
Biochem. Biophys. Res. Commun. 239, 386-392, 1997  
A:Title: Molecular cloning of a novel brain-specific serine protease with a kring-like  
A:Reference number: JC5759; MUID:98008848; PMID:9344839  
A:Accession: JC5759  
A:Molecule type: mRNA  
A:Residues: 1-761 <YAM>  
A:Cross-references: DDBJ:D89871  
A:Experimental source: brain  
C:Superfamily: brain-specific serine protease; scavenger receptor cysteine-rich domain  
F:85-157/Domain: kring-like #status predicted <KRI>  
F:163-266/Domain: scavenger receptor cysteine-rich domain homology <SRC7>  
F:166-266,273-372,386-486/Domain: scavenger receptor cysteine-rich #status predicted <SRC>  
F:513-516/Domain: furin binding #status predicted <FRB>  
F:517-755/Domain: trypsin homology <TRY>  
F:93,521,569/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:562,612,711/Active site: His, Asp, Ser #status predicted

Query Match 21.6%; Score 527; DB 2; Length 761;  
Best Local Similarity 31.9%; Pred. No. 2.3e-34; Indels 118; Gaps 21;  
Matches 147; Conservative 53; Mismatches 143

70 HFD-----CSGKYRCRSPFKIELIARCDGVSDCKDGED----- 103  
326 HFDGSRPIWLDVSCSGK---EVSP--IQCSRRQWRGHDCSHREDVGLATCYPDSGDHRL 380  
104 --EYRCVRVGGQ---AVLQVFTAAWKTCSDDKWKHYANVACAQIGFP-----SY 150  
381 SPGFPIRLVDGNGKGEVFEVNGQWGTICDDGWTDKHAAVTCRLQYKGPAPARTMAY 440  
151 -----VSSDNLRLVSLEGQRFBEFVSIDHLLPDDKVTALHRSV-----VYREGCAS 196  
441 FPEGKGPIMHNDVKTG-----NEKALADCVKQDIGHNCRHSDAGVICDYLEKKASS 494  
197 GHVVTLOCTAG---HRRGYSRRIVGNNMLLSQWPAQSLQFGYH-----LCGGSVI 247  
495 SGNKEMLSGGGLRLHRR--QKRIIGNNLSRGAWPQASRLRSARHGDRLLCGATLL 552  
248 TPLVITTAHCV-----YDLVLPKSWTIQVGLVSLLDNPAPSHLVEKIV 291  
553 SSCWLTAAHCFKRYGNNRSYAVRVGDYHTLVPEEPEQIG-----VQIV 599

292 YHSKYKPKRLGNDIALMKLAGP-----LTFNEMIQVCLPNSGEENFPD--GRVCWTSGMGA 345  
600 IHRNYPADSDYDIALVRLQGEQCARLSHTVLPAFLPWRER-POKTASNCHITGMD 658  
346 TEDGGDASPVLNHAAVPLNISKNICNHRDVTGGIISPSMLCAGYL--TGVDSQDSDGG 403  
659 T--GRAYSRTLQAAVAPLLPKRFCKER--YKGLFTGRMLCAGNLQEDNRVDSQDSDGG 714

404 LVCOE--RLWKLVGATSGFSGCAEVNKPVGVTYRTVTSFLDWI 443  
715 LMCEKPDSEWVYGVTSWVGCGVKDTPGVYTRVPAFVFI 755

RESULT 11  
A61545  
Plasmin (EC 3.4.21.7) precursor - horse (fragments)  
N:Alternate names: plasminogen  
N:Contains: miniplasminogen  
C:Species: Equus caballus (domestic horse)  
C:Date: 28-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 18-Jul-1997  
C:Accession: A61545; S17527  
R:Schaller, J.; Rickli, E.E.  
Enzyme 40, 63-69, 1988  
A:Title: Structural aspects of the plasminogen of various species.  
A:Reference number: A61545; MUID:89005015; PMID:3168975  
A:Accession: A61545  
A:Molecule type: protein  
A:Residues: 1-33;34-117 <SCH>  
R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.  
Protein Seq. Data Anal. 4, 69-74, 1991  
A:Title: Complete amino acid sequence of equine miniplasminogen.  
A:Reference number: S17527; MUID:92052077; PMID:1946332  
A:Accession: S17527  
A:Molecule type: protein  
A:Residues: 118-455 <SC2>  
C:Superfamily: plasmin; kring-like homology; plasminogen-related protein precursor homology;  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringlike; plasma; serine proteinase; z;  
F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>  
F:1-33/Domain: activation peptide (fragment) #status experimental <APT>  
F:118-455/Product: miniplasminogen #status experimental <MIN>  
F:37-114/Domain: kring-like homology <KRI>  
F:118-455/Domain: kring-like homology <KRI>  
F:126-205/Domain: plasmin chain B #status experimental <BCH>  
F:226-448/Domain: trypsin homology <TRY>  
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 21.5%; Score 526; DB 2; Length 455;  
Best Local Similarity 42.0%; Pred. No. 1.5e-34; Indels 14; Gaps 6;  
Matches 107; Conservative 47; Mismatches 87

203 OCTA---CG---HRRGYSRRIVGNNMLLSQWPAQSLQFQ-GYHLCGSGVITPLWII 253  
204 QCESSPFQGPCKVEPKCKSGRIVGGCVIAHSPWQISLSTRFGRHFCGTLISPEWVL 263  
254 TAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGP 313  
264 TAAHCLERSRSPSTYKVLGTHHELRLAAGAQQID--VSKLFLPESRA--DIALKLSSP 319  
314 LTFNEMIQVCLPNSGEENFPDQKVCWTSGGATDGGDASPVLNHAAVPLNISKNICHRD 373  
320 AITONVPIACLPADYVVAWAECEFTVGWETQDSSNAG-VLKEAQIPLVENKVCNRYE 378  
374 VYGGIISPSMLCAGYLIGVDSCQDSDGGLVLCVORRLWKLVGATSGFSGCAEVNKPVG 433  
379 YLNGRVKSTELCAGHLVGGVDSQDSDGGLVLCVCFEKDYKILQVGTWSGLGCARPKNPGV 438  
434 TRVTSFLDWIHEQME 448  
439 VRVSSFINWIERIMQ 453

RESULT 12



PLPG  
plasmin (EC 3.4.21.7) precursor - pig (fragment)  
N;Alternate names: plasminogen  
N;Contains: miniplasminogen  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 07-Sep-1990 #sequence\_revision 01-Nov-1996 #text\_change 18-Jul-1997  
C;Accession: S03733; R25834  
R;Schaller, J.; Marti, T.; Roessel, S.J.; Kaempfer, U.; Rickli, E.E.  
Fibrinolysis 1, 91-102, 1987  
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca  
A;Reference number: S03733  
A;Accession: S03733  
A;Molecule type: protein  
A;Residues: 1-560 <SCH>  
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mannenberg, M.;  
Eur. J. Biochem. 114, 465-470, 1981  
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,  
A;Reference number: S03735; MUID:81212097; PMID:7238497  
A;Accession: S03737  
A;Molecule type: protein  
A;Residues: 1-57 <BRU>  
R;Marti, T.; Schaller, J.; Rickli, E.E.  
Eur. J. Biochem. 149, 279-285, 1985  
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.  
A;Reference number: A25834; MUID:55203907; PMID:3846533  
A;Accession: A25834  
A;Molecule type: protein  
A;Residues: 450-790 <MAR>  
C;Function:  
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va  
ns the walls of the graafian follicle; also activates the u-kinase-type plasminogen act  
A;Pathway: fibrinolysis  
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote  
F;1-790/Product: plasminogen #status predicted <PRO>  
F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>  
F;1-77/Domain: activation peptide #status predicted <APT>  
F;78-560/Product: plasmin chain A #status predicted <ACH>  
F;84-162/Domain: kringle homology <KR1>  
F;166-243/Domain: kringle homology <KR2>  
F;256-333/Domain: kringle homology <KR3>  
F;359-435/Domain: kringle homology <KR4>  
F;450-790/Product: miniplasminogen #status experimental <MIN>  
F;461-540/Domain: kringle homology <KR5>  
F;561-790/Product: plasmin chain B #status experimental <BCH>  
F;561-793/Domain: trypsin homology <TRY>  
F;30-54.34-42.84-162.105-145.133-157.166-243.169-297.187-226.215-238.256-333.277-316.305  
bonds: #status predicted  
F;602.645.740/Active site: His, Asp, Ser #status predicted

Query Match 21.4%; Score 523.5; DB 1; Length 790;  
Best Local Similarity 41.4%; Pred. No. 4.6e-34;  
Matches 108; Conservative 43; Mismatches 89; Indels 21; Gaps 6;  
QY 194 CASGHVVTLOCTACGHRGYSRRIVGGNMLLSQWPQASLOFOGY--HLGGSVITPLW 251  
Db 547 CGKPKVEPKCPA-----RVVGGCVSIPHSWPMQISLRYR-YRGHFCGGLTSPW 596  
QY 252 IITAAHCVDVLYLPKSWTIQGLVSLDNPAPSHLVEKI--VHSHKPKRLGNDIALMK 309  
Db 597 VLTAKHCLKSSSSSSYKV-----ILGAHEYHLGEGVQEIYDKLFKPSHADIALK 650  
QY 310 LAGPLTFNEMIQVCLPNSNENFPDGKVCWTSGMGATEDGGDASPVLNHAAVPLISKNIC 369  
Db 651 LSSPAVITDKVIPACLPNTVAVDRTACYTITGWGETK-GTYGAGALLKEARLPVIEKNVC 709  
QY 370 NHRDVYGGIISPSMLCAGVLTGGVDSGCGSGLPVCCEERLWLKLVGATSGFGICAEVNYK 429  
Db 710 NRYELGKVSFNEICAGHLAGGIDSCGDSGGPLVCFEKKYILQGVTSWGLCALPNK 769  
QY 430 PGVYTRVTSFLDWIHEQMERD 450  
Db 770 PGVYVRVSRFVTWIEIMERN 790

RESULT 13  
JE0315  
low-density lipoprotein receptor-related protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Feb-2003  
C;Accession: JE0315  
R;Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.  
J. Biochem. 124, 784-789, 1998  
A;Title: A novel low-density lipoprotein receptor-related protein with type II membrane I  
A;Reference number: JE0315; MUID:98429596; PMID:9756624  
A;Accession: JE0315  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1113 <TOM>  
A;Cross-references: DBJ:AB013874; NID:93869144; PIDN:BA34371.1; PID:93869145  
C;Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor ligar  
F;337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F;374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F;410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F;484-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F;723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F;869-1097/Domain: trypsin homology <TRY>  
Query Match 20.7%; Score 506.5; DB 2; Length 1113;  
Best Local Similarity 31.7%; Pred. No. 1.6e-32;  
Matches 126; Conservative 76; Mismatches 160; Indels 35; Gaps 16;  
QY 72 DCS-----GKYCRSFFKCIELIARCDGVSDCKGDEYRCVRV---GGQNAVLOVFTTAA 124  
Db 719 NCSFQDNELEC-ANHECVPRDLWCDDGWDCSDSDSEMGCVTLTKNGNSLLTVHKSAAK 777  
QY 125 WKTMSDDWKHYANVACAQLG--PSVSSDNLVRSLEQGFEEFVSIDHLLPDDKVT 182  
Db 778 EHVACDQWRETLSQLACKQMLGEPVS-----TKLIPQEGCQQLURIPNWNENLNGS 830  
QY 183 ALHSHVYVREGCASGHVVTLOCTA--CGHRRG--YSSRIVGGNMLLSQWPQASLOFQ- 237  
Db 831 TLQELLVYHSCPSRSESLSCSKODCGRRPAARMNKILGRTSRPGRNFWQCSLOSEP 890  
QY 238 GYHLCGGSVITPLWITIAHCVDVLYLPKSWTIQGLVSLDNPAA--PSHLVEKIVVHS 294  
Db 891 SGHICGCVLLAKKWLTVHACFEGRDADVMKVFEG--INNLDHPGSGFMQTRFVKILLHP 949  
QY 295 KYKPKRLGNDIALMKLAGPLTFNEMIQVCLPNSNENFPDGKVCWTSGMGATEDGGDASP 354  
Db 950 YSRAVVDYDISVVELSDIDNETSVRPVCLPSPPEYLEPDTYCYITCGHM--GNKMP 1006  
QY 355 V-INHAAVPLISKNIC-NHRDVYGGIISPSMLCAGVLTGGVDSGCGSGLPVCQD-RRL 411  
Db 1007 FKLQEGEVRIIPLEQCQSYFDM--KTIITRMICAGYESGTVDSCMGDSGGLVCRPGQ 1064  
QY 412 WKLVGATSGFGIC-AEVNKPQVYTRVTSFLDWIHEQM 447  
Db 1065 WTLFGLTSGVSCVFSKVLGPGVYSNVSIFVGWIERQI 1101

RESULT 14  
A47246  
Cryptase (EC 3.4.21.59) 2 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C;Accession: A47246  
R;McNeill, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.;  
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992  
A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast  
A;Reference number: A47246; MUID:93087489; PMID:1454796  
A;Accession: A47246  
A;Status: preliminary  
A;Molecule type: nucleic acid

